SEQUENCE LISTING

(1) GENERAL INFORMATION:
   (i) APPLICANTS:

        BERGERON, Michel G. [1], 1145 des Érables, Québec City, Québec, Canada, G2K 1T8
        BOISSINOT, Maurice [1], 109 Jean-Bruchési, St-Augustin-de-Desmaures, Québec, Canada, G3A 2N2
        HULETSKY, Ann [1], 1231 Av des Pins, Sillery, Québec, Canada, G1S 4J3
        MÉNARD, Christian [1], 1174 Rue du Pont, St-Lambert-de-Lévis, Québec, Canada, G0S 2W0
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        PICARD, François J. [1], 1245 de la Sapinière, Cap-Rouge, Québec, Canada, G1Y 1A1
        ROY, Paul H. [2], 28 Charles Garnier, Loretteville, Québec, Canada, G2A 2X8

       [1]: Canadian citizenship
       [2]: American citizenship

   (ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL, FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

   (iii) NUMBER OF SEQUENCES: 2297

   (iv) CORRESPONDENCE ADDRESS:

      (A)   ADDRESSEE:
      (B)   STREET:
      (C)   CITY:
      (D)   STATE:
      (E)   COUNTRY:
      (F)   ZIP:

   (v) COMPUTER READABLE:

      (A)   MEDIUM TYPE:
      (B)   COMPUTER:
      (C)   OPERATING:
      (D)   SOFTWARE:

   (vi) CURRENT APPLICATION DATA:

      (A)   APPLICATION:
      (B)   FILING DATE:
      (C)   CLASSIFICATION:

   (vii) PRIOR APPLICATION DATA:

      (A)   APPLICATION:
      (B)   FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

      (A)   NAME:
      (B)   REGISTRATION NUMBER:

5

  (ix) TELECOMMUNICATION INFORMATION:
      (A)   TELEPHONE:
      (B)   TELEFAX:

2

2) INFORMATION FOR SEQ ID NO: 1

    (i) SEQUENCE CHARACTERISTICS:
5
        (A)   LENGTH: 750 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

10   (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Acinetobacter baumannii*
        (B)   STRAIN: ATCC 19606
15
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

```
     CAAACTCGTG  AGCACATCCT  TCTTTCTCGT  CAGGTAGGTG  TACCTTACAT      50
     CATCGTATTC  TTAAACAAAT  GCGACCTTGT  TGATGACGAA  GAATTACTTG     100
20   AATTAGTAGA  AATGGAAGTA  CGTGAACTTC  TTTCTACTTA  TGACTTCCCA     150
     GGTGATGACA  CTCCAGTAAT  CCGTGGTTCA  GCTCTTGCAG  CGCTTAACGG     200
     TGAAGCTGGT  CCTTACGGTG  AAGAATCAGT  TCTTGCTCTT  GTAGCAGCAC     250
     TTGACTCTTA  CATCCCAGAG  CCAGAGCGTG  CAATCGACAA  AGCATTCTTG     300
     ATGCCAATCG  AAGACGTATT  CTCAATTTCT  GGTCGTGGTA  CAGTAGTAAC     350
25   AGGCCGTGTT  GAAGCTGGTA  TCATCAAAGT  TGGTGAAGAA  GTAGAGATCG     400
     TTGGTATTAA  AGATACAGTT  AAAACAACTG  TAACTGGCGT  AGAAATGTTC     450
     CGTAAACTTC  TTGACGAAGG  CCGTGCAGGT  GAGAACTGTG  GTATCTTACT     500
     TCGTGGTACT  AAGCGTGAAG  AAGTACAACG  TGGTCAAGTA  CTTGCTAAAC     550
     CAGGTACAAT  CAAGCCGCAC  ACTAAATTCG  ACGCAGAAGT  ATACGTACTT     600
30   TCTAAAGAAG  AAGGTGGTCG  TCACACTCCA  TTCTTAAATG  GTTACCGTCC     650
     ACAGTTCTAC  TTCCGTACAA  CTGACGTAAC  TGGTGCRATC  CAGTTGAAAG     700
     AAGGCGTTGA  AATGGTAATG  CCAGGTGACA  ACGTTGAAAT  GTCAGTAGAA     750
```

35
2) INFORMATION FOR SEQ ID NO: 2

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 826 bases
40   (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA
45
    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Actinomyces meyeri*
        (B)   STRAIN: ATCC 35568

50   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

```
     CGGTGCGATC  CTCGTGGTCG  CCGCGACCGA  CGGCCCCATG  GCCCAGACCC      50
     GCGAGCACGT  CCTGCTCGCC  CGTCAGGTCG  GCGTTCCCAC  CATCCTCATC     100
     GCCCTCAACA  AGTCCGACAT  GGTTGACGAC  GAGGAAATGA  TGGAACTGGT     150
55   CGAGGAGGAG  TGCCGCGACC  TGCTGGAGTC  CCAGGACTTC  GATCGCGATG     200
     CCCCGATCGT  CCAGGTTTCC  GCTCTGAAGG  CCCTCGAGGG  CGACGCGGAG     250
     TGGGTTGCCA  AGATCGAGGA  GCTCATGGAG  GCTGTGGATT  CCTACATCCC     300
     CACCCCCGAG  CGCGATATGG  ACAAGCCCTT  CCTCATGCCG  ATCGAGGACG     350
     TCTTCACGAT  CACAGGTCGT  GGCACGGTCG  TCACGGGGCG  TGTTGAGCGT     400
60   GGCAAGCTGC  CGATCAACTC  CGAGGTCGAG  ATCCTCGGTA  TCCGTGATCC     450
```

```
CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG          500
AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC          550
GATGAGGTTG AGCGCGGCCA GGTTGTGGCC ATTCCCGGCT CCATCACGCC          600
TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG          650
GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT          700
ACCACGGACG TGACCGGCGT CATCACCCTC CCCGAGGGCA CCGACATGGT          750
CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG          800
CCATGGAGCC CGGCTGGGCT TCGCCA                                    826
```

2) INFORMATION FOR SEQ ID NO: 3

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 835 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

   (ii) MOLECULE TYPE: Genomic DNA

   (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Aerococcus viridans*
       (B)   STRAIN: ATCC 11563

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

```
TGGTGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC           50
GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTTCCTGC ATTCGTAGTA          100
TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT          150
TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG          200
ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA          250
GCTCAAGAAG CTAAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT          300
TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG          350
ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA          400
CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA          450
ACAAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTC CGTAAAAACT          500
TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGTT          550
CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT          600
CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG          650
AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC          700
TTCCGTACTA CTGACATTAC TGGTGTTATC ACTTTACCAG AAGACGTAGC          750
TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCACC          800
CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC                          835
```

2) INFORMATION FOR SEQ ID NO: 4

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 827 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

   (ii) MOLECULE TYPE: Genomic DNA

   (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Achromobacter xylosoxidans* subsp.
      denitrificans

4

(B)   STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

```
5    CCTGGTGGTG TCGGCCGCTG ACGGCCCGAT GCCGCAAACG CGCGAACACA        50
     TCCTGCTGAG CCGCCAGGTT GGCGTGCCGT ACATCATCGT CTTCCTGAAC        100
     AAGGCCGACA TGGTTGACGA CGCCGAGCTG CTTGAGCTGG TGGAAATGGA        150
     AGTTCGCGAR CTGCTGAGCA AGTACGACTT CCCGGGCGAC GACACCCCGA        200
     TCGTGAAGGG TTCGGCCAAG CTGGCGCTGG AAGGCGACAA GGGCGAACTG        250
10   GGCGAACAGG CCATCATGGC GCTGGCCGCT GCGCTGGACT CGTACATCCC        300
     GACGCCTGAG CGTGCCGTTG ACGGCGCGTT CCTGATGCCG GTTGAAGACG        350
     TGTTCTCGAT CTCGGGTCGC GGCACCGTGG TGACCGGCCG TATCGAACGC        400
     GGCATCATCA AGGTCGGCGA GGAAATCGAA ATCGTCGGTC TGGTGCCGAC        450
     GGTGAAGACG ACCTGCACGG GCGTGGAAAT GTTCCGCAAG CTGCTGGACC        500
15   AAGGTCAAGC CGGCGACAAC GTGGGCATCC TRCTGCGCGG CACCAAGCGT        550
     GAAGACGTCC AGCGCGGCCA GGTTCTGGCC AAGCCGGGCT CGATCACCCC        600
     GCACACGGAC TTCACGTCCG AGGTGTACAT CCTGTCCAAG GAAGAAGGCG        650
     GCCGTCACAC TCCGTTCTTC CAAGGCTATC GTCCCCAGTT CTACTTCCGC        700
     ACGACGGACG TGACGGGCAC GATCGAGCTG CCGGCCGACA AGGAAATGGT        750
20   CCTGCCGGGC GACAACGTGG CCATGACGGT CAAGCTGCTG GCTCCGATCG        800
     CCATGGAAGA AGGCCTGCGT TCGCCAC                                827
```

25   2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:
    (A)   LENGTH: 823 bases
    (B)   TYPE: Nucleic acid
30   (C)   STRANDEDNESS: Double
    (D)   TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35   (vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Anaerorhabdus furcosus*
    (B)   STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5
40

```
     TGGATCAATC CTAGTAGTTG CTGCAACTGA TGGACCAATG CCTCAAACTC        50
     GTGAACATAT CTTACTTGCT CGTCAAGTAG GTGTTCCAAG AATGGTTGTA        100
     TTCTTGAACA AATGCGACAT GGTTGAAGAT GAAGAATTAA TCGACCTTGT        150
     TGAAATGGAA GTTCGTGAAC TTCTAAGTGC TTACGGTTTC GAAGGTGATG        200
45   ATACACCAGT TATCCGTGGT TCTGCATTAA AATCTCTTGA AGGAAATGCT        250
     GATTGGGAAG CAAAAGTTGC TGAATTAATG GATGCAGTTG ACTCTTGGAT        300
     TCCAACTCCA ACTCATGAAA CAGACAAACC ATTCTTAATG GCTGTTGAAG        350
     ATGTATTCAC AATTACAGGT CGTGGTACAG TTGCTACTGG ACGTGTTGAA        400
     CGTGGACACT TAAACCTTAA CGAAGAAGTT GAAATCGTTG GTATTCATGA        450
50   TACTAAGAAA TCAGTTGTTA CTGGTATCGA AATGTTCCGT AAATTATTAG        500
     ACTATGCTGA AGCAGGAGAC AACATTGGTG CATTATTACG TGGTGTTTCT        550
     CGTGATGAAA TCGAACGTGG ACAATGTCTA GCTAAACCTG GATCAGTTAC        600
     TCCACATACA GCTTTCAAAG CTCAAGTATA CGTATTAACT AAAGAAGAAG        650
     GTGGACGTCA TACACCATTC GTAACTAACT ACCGTCCTCA ATTCTATTTC        700
55   CGTACAACTG ACGTAACAGG AGTTGTTAAA CTTCCTGAAG GTACTGAAAT        750
     GGTTATGCCT GGAGACAACA TCGAAATGAT CGTTGAATTA ATCGCTCCAA        800
     TCGCTGTTGA ACAAGGAACT AAG                                    823
```

60

5

2) INFORMATION FOR SEQ ID NO: 6

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 825 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Bacillus anthracis*
       (B)   STRAIN: 4229

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

```
CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACTC    50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTACCTTA CATCGTTGTA    100
TTCTTAAACA AATGCGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT    150
AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG    200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT    250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT    300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG    350
ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG    400
CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA    450
AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC    500
TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT    550
GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT    600
AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG    650
AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC    700
TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA    750
AATGGTAATG CCTGGTGACA ACATCGAAAT GACTATCGAA CTTATCGCTC    800
CAATCGCTAT CGAAGAGGGA ACTAA                               825
```

2) INFORMATION FOR SEQ ID NO: 7

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 829 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Bacillus cereus*
       (B)   STRAIN: ATCC 14579

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

```
CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACAC    50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTTCCTTA CATCGTTGTA    100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAATTAT TAGAATTAGT    150
AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG    200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT    250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT    300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG    350
ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG    400
```

```
      CGCGGTATCG  TTAAAGTTGG  TGACGTAGTA  GAAATCATCG  GTCTTGCTGA    450
      AGAAAATGCT  TCTACAACTG  TAACTGGTGT  AGAGATGTTC  CGTAAACTTC    500
      TTGACCAAGC  TCAAGCTGGA  GACAACATCG  GTGCTTTACT  TCGTGGGGTT    550
      GCTCGTGAAG  ACATCCAACG  TGGACAAGTA  CTTGCAAAAA  GCGGTTCTGT    600
   5  AAAAGCTCAC  GCTAAATTCA  AAGCTGAAGT  TTTCGTATTA  TCTAAAGAAG    650
      AAGGTGGACG  TCACACTCCA  TTCTTCGCTA  ACTACCGTCC  TCAGTTCTAC    700
      TTCCGTACAA  CTGACGTAAC  TGGTATCATC  CAATTACCAG  AAGGTACTGA    750
      AATGGTAATG  CCTGGTGACA  ACATTGAAAT  GACTATCGAA  CTTATCGCTC    800
      CAATCGCTAT  CGAAGAGGGA  ACTAAATTC                            829
  10
```

2) INFORMATION FOR SEQ ID NO: 8

  15   (i) SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 818 bases
              (B)   TYPE: Nucleic acid
              (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear

  20   (ii) MOLECULE TYPE: Genomic DNA

         (vi) ORIGINAL SOURCE:
              (A)   ORGANISM: *Bacteroides distasonis*
  25   (B)   STRAIN: ATCC 8503

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

```
      CGGTGCTATC  ATCGTAGTTG  CTGCTACTGA  TGGTCCTATG  CCTCAAACTC     50
  30  GCGAGCACAT  CCTTTTGGCT  CGTCAGGTAA  ACGTTCCGAG  ATTGGTTGTA    100
      TTCATGAACA  AGTGTGACAT  GGTTGACGAC  GAGGAAATGT  TGGAATTGGT    150
      TGAGATGGAG  ATGAGAGAGT  TGCTTTCATT  CTATCAATTC  GACGGTGACA    200
      ACACTCCGAT  CATCCGTGGT  TCTGCTCTTG  GTGCATTGAA  CGGTGATGCT    250
      CAATGGGAAG  ATAAAGTAAT  GGAGTTGATG  GAAGCTTGTG  ATACTTGGAT    300
  35  TCCTCTGCCT  CCGCGCGAAA  TCGACAAGCC  GTTCTTGATG  CCGGTTGAGG    350
      ACGTATTCTC  AATCACGGGT  CGTGGTACTG  TTGCTACAGG  TCGTATCGAG    400
      ACAGGTATTG  TTAAGGTTGG  TGAGGAAGTT  CAGATCATCG  GTCTTGGCGC    450
      TGCTGGTAAG  AAATCTGTTG  TTACAGGTGT  TGAGATGTTC  CGTAAGTTAT    500
      TGGATCAAGG  TGAGGCTGGT  GATAACGTTG  GTTTGTTGCT  TCGCGGTATC    550
  40  GATAAGAATG  AGATCAAGCG  TGGTATGGTA  ATCTGCCACC  CGGGTCAGGT    600
      TAAAGAGCAT  TCTAAGTTCA  AGGCTGAGGT  TTATATCTTG  AAGAAAGAGG    650
      AAGGTGGTCG  TCACACTCCG  TTCCACAACA  AATATCGTCC  TCAGTTCTAT    700
      ATCCGTACAT  TGGATGTAAC  TGGTGAGATC  ACTTTGCCGG  AAGGAACTGA    750
      AATGGTAATG  CCGGGTGATA  ACGTAACGAT  CGAGGTTGAG  TTGATCTATC    800
  45  CGGTAGCATG  TAGCGTAG                                          818
```

2) INFORMATION FOR SEQ ID NO: 9
  50
         (i) SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 639 bases
              (B)   TYPE: Nucleic acid
              (C)   STRANDEDNESS: Double
  55   (D)   TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
  60   (A)   ORGANISM: *Enterococcus casseliflavus*

     (B)   STRAIN: R763

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

```
 5   GGTCCTATGC CTCAAACACG TGAACACATC TTGTTATCAC GTAACGTTGG    50
     TGTACCATAC ATCGTTGTTT TCTTAAACAA AATGGATATG GTTGATGACG   100
     AAGAATTACT AGAATTAGTT GAAATGGAAG TTCGTGACTT ATTGTCAGAA   150
     TATGACTTCC CAGGCGACGA TGTTCCTGTA ATCGCTGGTT CTGCTTTGAA   200
     AGCTCTTGAA GGCGATGCTT CATACGAAGA AAAAATCATG GAATTAATGG   250
10   CTGCAGTTGA CGAATACGTT CCAACTCCAG AACGTGACAC TGACAAACCA   300
     TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT   350
     TGCTACAGGC CGTGTTGAAC GTGGACAAGT TCGCGTTGGT GACGAAGTTG   400
     AAATCGTTGG TATTGCTGAA GAAACTGCTA AAACAACTGT AACTGGTGTT   450
     GAAATGTTCC GTAAATTGTT AGACTATGCT GAAGCAGGGG ATAACATTGG   500
15   TGCATTGCTA CGTGGTGTTG CTCGTGAAGA CATCCAACGT GGACAAGTAT   550
     TGGCTAAAGC TGGTACAATC ACACCTCATA CAAAATTTAA AGCTGAAGTT   600
     TACGTTTTAA CAAAAGAAGA AGGTGGACGT CACACACCA              639
```

20
2) INFORMATION FOR SEQ ID NO: 10

   (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 692 bases
25   (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

   (ii) MOLECULE TYPE: Genomic DNA
30
   (vi) ORIGINAL SOURCE:
      (A)   ORGANISM: *Staphylococcus saprophyticus*
      (B)   STRAIN: CSG 197

35   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

```
     GAACACATTC TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT    50
     CTTAAACAAA GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG   100
     AAATGGAAGT TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT   150
40   GTACCTGTAA TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA   200
     CTATGAGCAA AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC   250
     CAACACCAGA ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC   300
     GTATTCTCAA TCACTGGTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG   350
     TGGTCAAATC AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG   400
45   AATCAAGCAA AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA   450
     GACTACGCTG AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTTC   500
     ACGTGATGAC GTACAACGTG GTCAAGTTTT AGCTGCTCCT GGTACTATTA   550
     CACCACATAC AAAATTCAAA GCGGATGTTT ACGTTTTATC TAAAGATGAA   600
     GGTGGTCGTC ATACACCATT CTTCACTAAC TACCGCCCAC AATTCTATTT   650
50   CCGTACTACT GACGTAACTG GTGTTGTTAA CTTACCAGAA GG           692
```

2) INFORMATION FOR SEQ ID NO: 11
55
   (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 821 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
60   (D)   TOPOLOGY: Linear

8

```
     (ii)MOLECULE TYPE: Genomic DNA

     (vi)ORIGINAL SOURCE:
5          (A)    ORGANISM: Bacteroides ovatus
           (B)    STRAIN: ATCC 8483

     (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 11

10   CGGTGCTATC ATCGTTTGTG CTGCAACTGA TGGTCCGATG CCTCAAACTC        50
     GCGAACACAT TCTGTTAGCT CGTCAGGTAA ACGTACCTCG TCTGGTTGTA       100
     TTCTTGAACA AATGCGATAT GGTAGACGAC GAAGAAATGT TGGAACTCGT       150
     TGAAATGGAA ATGAGAGAAC TCCTTTCATT CTATGATTTC GATGGTGACA       200
     ATACTCCTAT CATCCGTGGT TCTGCTCTTG GCGCATTGAA CGGTGTTGAA       250
15   AAATGGGAAG ACAAAGTTAT GGAACTGATG GATGCAGTTG ATAACTGGAT       300
     TCCACTGCCT CCGCGCGATG TTGATAAACC ATTCTTGATG CCGGTTGAAG       350
     ACGTGTTCTC TATCACAGGT CGTGGTACTG TAGCAACAGG TCGTATCGAA       400
     ACAGGTGTCA TCCACGTTGG TGATGAAGTC GAAATTCTTG GTTTAGGTGA       450
     AGATAAGAAA TCAGTTGTAA CTGGTGTTGA AATGTTCCGT AAACTGTTGG       500
20   ATCAAGGTGA AGCTGGTGAC AACGTAGGTC TTTTGCTTCG TGGTATTGAC       550
     AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAACCAG GTCAGATTAA       600
     ACCGCACTCT AAATTCAAAG CTGAGGTTTA TATCTTGAAG AAAGAAGAAG       650
     GTGGTCGTCA CACTCCGTTC CACAACAAAT ACCGTCCTCA GTTCTACTTG       700
     CGTACTATGG ACTGTACAGG TGAAATCACT TTGCCGGAAG GAACAGAAAT       750
25   GGTAATGCCG GGTGATAACG TAACTATTAC AGTTGAGTTG ATTTACCCAG       800
     TAGCATTGAA CCCGGGCTTC G                                      821



30   2)INFORMATION FOR SEQ ID NO: 12

        (i)SEQUENCE CHARACTERISTICS:
           (A)    LENGTH: 838 bases
           (B)    TYPE: Nucleic acid
35         (C)    STRANDEDNESS: Double
           (D)    TOPOLOGY: Linear

     (ii)MOLECULE TYPE: Genomic DNA

40   (vi)ORIGINAL SOURCE:
           (A)    ORGANISM: Bartonella henselae
        (B)       STRAIN: ATCC 49882

     (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 12
45
     TGGTGCGATT TTGGTTGTTT CAGCTGCTGA TGGTCCGATG CCTCAAACAC        50
     GTGAGCATAT TCTTCTTGCC CGTCAGGTTG GTGTTCCAGC GATTGTTGTT       100
     TTTCTTAATA AGGTTGATCA GGTTGATGAT GCTGAGCTTT TGGAGCTTGT       150
     TGAGCTTGAA GTTCGGGAGT TATTGTCGAA ATATGATTTT CCAGGAGACG       200
50   ATATTCCGAT CGTTAAAGGT TCTGCTTTGG CAGCGCTTGA AGATAAAGAT       250
     AAAAGCATTG GTGAAGATGC GGTTCGTCTT TTGATGAGTG AAGTTGATAA       300
     TTATATACCG ACGCCTGAAC GTCCTGTTGA TCAGCCGTTT TTGATGCCAA       350
     TTGAAGATGT TTTTTCGATT TCGGGTCGTG GAACTGTTGT GACGGGTCGT       400
     GTTGAGCGTG GTGTTATTAA GGTTGGTGAA GAAGTTGAGA TTATCGGCAT       450
55   TCGTCCAACT TCTAAGACAA CAGTTACAGG GGTTGAAATG TTCCGCAAGC       500
     TTTTAGATCA GGGGCAAGCG GGTGATAATA TTGGAGCGCT GCTTCGTGGT       550
     ATTGATCGTG AAGGGATTGA GCGTGGACAA GTTTTGGCGA AGCCTGCTTC       600
     GGTTACACCT CATACGAGAT TTAAAGCAGA GGCTTACATT TTGACGAAAG       650
     ATGAAGGTGG TCGTCATACT CCATTTTTCA CGAATTATCG TCCTCAGTTT       700
60   TATTTCCGTA CTACGGATGT AACGGGAATT GTTACGCTTC CAGAAGGTAC       750
```

```
AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG          800
TTCCAATTGC CATGGAAGAA AAACTTCGTT TTGCTATC                       838
```

2) INFORMATION FOR SEQ ID NO: 13

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 839 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Bifidobacterium adolescentis*
       (B)   STRAIN: ATCC 15703

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

```
TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC          50
GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC          100
GCTCTGAACA AGTGCGATAT GGTCGACGAC GACGAGCTCA TCGAGCTCGT          150
TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT          200
GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG          250
GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA          300
TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC          350
CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC          400
CGTGTCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG          450
CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA          500
AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC          550
GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG          600
CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA          650
AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG          700
TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG          750
CGTTGAGATG GTGCAGCCGG CGATCACGC TACCTTCGGC GTTGAGCTGA           800
TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG                      839
```

2) INFORMATION FOR SEQ ID NO: 14

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 839 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Bifidobacterium dentium*
       (B)   STRAIN: ATCC 27534

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

```
TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC          50
GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC          100
GCCCTGAACA AGTGCGATAT GGTCGACGAC GAAGAGCTCA TCGAGCTCGT          150
```

10

```
     TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAACGGCTTC GATCGCGATT         200
     GCCCGGTCAT CCACACCTCC GCCTACGGCG CGCTGCACGA TGACGCTCCG         250
     GACCACGACA AGTGGGTTGA GTCCGTCAAG GAACTCATGA AGGCCGTCGA         300
     CGAGTACATC CCGACCCCGA CCCACGATCT GGACAAGCCG TTCCTGATGC         350
 5   CGATCGAAGA TGTGTTCACC ATCTCCGGCC GTGGCACCGT GGTTACCGGC         400
     CGTGTCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTTG AGATCGTCGG         450
     CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA         500
     AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC         550
     GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG         600
10   CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA         650
     AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG         700
     TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG         750
     CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA         800
     TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG                     839
15
```

2) INFORMATION FOR SEQ ID NO: 15

20   (i) SEQUENCE CHARACTERISTICS:
             (A)   LENGTH: 838 bases
             (B)   TYPE: Nucleic acid
             (C)   STRANDEDNESS: Double
             (D)   TOPOLOGY: Linear
25
        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
             (A)   ORGANISM: *Brucella abortus*
30   (B)   STRAIN: S2308

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

```
     TGGCGCGATC CTGGTGGTTT CGGCTGCTGA CGGCCCGATG CCGCAGACCC          50
35   GCGAGCACAT CCTGCTTGCC CGTCAGGTTG GCGTTCCGGC GATCGTCGTG         100
     TTCCTCAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT         150
     TGAACTGGAA GTGCGCGAAC TTCTGTCGAA GTACGAATTC CCCGGCGACG         200
     AAATCCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCC         250
     AAGGAACTGG GCGAAGATGC CATCCGCAAC CTGATGGACG CGGTTGACAG         300
40   CTACATTCCG ACCCCGGAAC GCCCGATCGA CCAGCCGTTC CTGATGCCGA         350
     TCGAAGACGT GTTCTCGATC TCCGGCCGTG GTACGGTTGT GACGGGTCGC         400
     GTTGAGCGCG GTATCGTTAA GGTCGGTGAA GAAGTTGAAA TCGTCGGCAT         450
     CAAGGCGACG ACGAAGACCA CGGTTACCGG CGTTGAAATG TTCCGCAAGC         500
     TGCTCGACCA GGGCCAGGCT GGCGACAACA TTGGCGCGCT GATCCGCGGC         550
45   GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTC         600
     TGTGAAGCCG CACACCAAGT TTAAGGCAGA AGCCTATATT CTGACCAAGG         650
     ACGAAGGTGG CCGTCATACG CCGTTCTTCA CCAACTACCG TCCGCAGTTC         700
     TACTTCCGTA CGACGGACGT GACGGGTGTT GTGACGCTTC CGGCTGGCAC         750
     GGAAATGGTC ATGCCTGGCG ATAACGTCGC CATGGACGTT ACCCTGATCG         800
50   TGCCGATCGC CATGGAAGAG AAGCTTCGCT TCGCTATC                      838
```

2) INFORMATION FOR SEQ ID NO: 16

55   (i) SEQUENCE CHARACTERISTICS:
             (A)   LENGTH: 771 bases
             (B)   TYPE: Nucleic acid
             (C)   STRANDEDNESS: Double
60   (D)   TOPOLOGY: Linear

                                    11

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Burkholderia cepacia*
    (B)   STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

```
GGCAGCAGAC GGCCCGATGC CGCAAACGCG TGAGCACATC CTGCTGGCGC      50
GTCAGGTTGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA GTGCGACATG     100
GTGGACGACG CCGAACTGCT CGAGCTGGTC GAGATGGAAG TTCGCGAACT     150
CCTGTCGAAG TACGACTTCC CGGGCGACGA CACGCCGATC GTGAAGGGTT     200
CGGCGAAGCT GGCGCTGGAA GGCGACACGG GCGAGCTGGG CGAAGTGGCG     250
ATCATGAGCC TGGCCGACGC GCTGGACACG TACATCCCGA CGCCGGAGCG     300
TGCAGTTGAC GGCGCGTTCC TGATGCCGGT GGAAGACGTG TTCTCGATCT     350
CGGGCCGCGG TACGGTGGTG ACGGGTCGTG TCGAGCGCGG CATCGTGAAG     400
GTCGGCGAAG AAATCGAAAT CGTCGGTATC AAGCCGACGG TGAAGACGAC     450
CTGCACGGGC GTTGAAATGT TCCGCAAGCT GCTGGACCAA GGTCAAGCAG     500
GCGACAACGT TGGTATCCTG CTGCGCGGCA CGAAGCGTGA AGACGTGGAG     550
CGTGGCCAGG TTCTGGCGAA GCCGGGTTCG ATCACGCCGC ACACGCACTT     600
CACGGCTGAA GTGTACGTGC TGAGCAAGGA CGAAGGCGGC CGTCACACGC     650
CGTTCTTCAA CAACTACCGT CCGCAGTTCT ACTTCCGTAC GACGGACGTG     700
ACGGGCTCGA TCGAGCTGCC GAAGGACAAG GAAATGGTGA TGCCGGGCGA     750
CAACGTGTCG ATCACGGTGA A                                    771
```

2) INFORMATION FOR SEQ ID NO: 17

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 829 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Cedecea davisae*
    (B)   STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

```
GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTTGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTA     150
GAAATGGAAG TTCGTGAACT TCTGTCCCAG TACGACTTCC CGGGCGACGA     200
TACTCCAATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGAAGCAG     250
AGTGGGAAGC TAAAATCGTT GAGCTGGCTG GCTACCTGGA TTCTTACATC     300
CCTGAGCCAG AGCGTGCTAT CGATAAGCCG TTCCTGCTGC CAATCGAAGA     350
CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT     450
ACTGCGAAAT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCAGG CTCTATCAAG     600
CCACACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC     700
GTACAACTGA CGTGACCGGC ACCATCGAAC TGCCAGAAGG CGTTGAGATG     750
GTAATGCCTG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT     800
```

12

CGCGATGGAT GACGGTCTGC GTTTCGCAA

5   2)INFORMATION FOR SEQ ID NO: 18

         (i)SEQUENCE CHARACTERISTICS:
             (A)   LENGTH: 824 bases
             (B)   TYPE: Nucleic acid
10   (C)   STRANDEDNESS: Double
             (D)   TOPOLOGY: Linear

         (ii)MOLECULE TYPE: Genomic DNA

15   (vi)ORIGINAL SOURCE:
             (A)   ORGANISM: *Cedecea neteri*
             (B)   STRAIN: ATCC 33855

         (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 18
20

CGCTATCCTG GTTGTTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG   50
AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC   100
CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA   150
AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGACTTCCCG GGCGATGACA   200
25 CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG   250
TGGGAAGCTA AAATYGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC   300
AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG   350
TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC   400
GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC   450
30 TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG   500
AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT   550
GAAGAAATCG AACGTGGTCA GGTTCTGGCT AAGCCAGGCT CTATCAAGCC   600
GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG   650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT   700
35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT   750
AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG   800
CGATGGACGA CGGTCTGCGT TTCG   824

40
2)INFORMATION FOR SEQ ID NO: 19

         (i)SEQUENCE CHARACTERISTICS:
             (A)   LENGTH: 827 bases
45   (B)   TYPE: Nucleic acid
             (C)   STRANDEDNESS: Double
             (D)   TOPOLOGY: Linear

         (ii)MOLECULE TYPE: Genomic DNA
50
         (vi)ORIGINAL SOURCE:
             (A)   ORGANISM: *Cedecea lapagei*
             (B)   STRAIN: ATCC 33432

55   (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCTG GTTGTTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG   50
AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTC   100
CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA   150
60 AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGACTTCCCA GGCGATGATA   200

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```
CCCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG        250
TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC        300
AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG        350
TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCG TGTAGAGCGC        400
GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC        450
TGCGAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG        500
AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT        550
GAAGAAATCG AACGTGGTCA GGTTCTGGCT AAGCCAGGCT CTATCAAGCC        600
GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG        650
GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT        700
ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT        750
AATGCCAGGT GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG        800
CGATGGACGA CGGTCTGCGT TTCGCAA                                 827
```

2) INFORMATION FOR SEQ ID NO: 20

```
   (i) SEQUENCE CHARACTERISTICS:
       (A)    LENGTH: 831 bases
       (B)    TYPE: Nucleic acid
       (C)    STRANDEDNESS: Double
       (D)    TOPOLOGY: Linear

   (ii) MOLECULE TYPE: Genomic DNA

   (vi) ORIGINAL SOURCE:
       (A)    ORGANISM: Chlamydia pneumoniae
       (B)    STRAIN: CWL 029

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20
```

```
GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAAACT         50
AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT        100
TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG        150
ACCTTGTTGA GATGGAACTT AGTGAGCTTC TTGAAGAAAA AGGCTACAAA        200
GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC        250
AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA        300
TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA        350
GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA        400
GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG        450
AGACTAAAGA AACAATCGTT ACTGGAGTCG AAATGTTCAG GAAAGAACTT        500
CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTACTCCTCA GAGGTATTGG        550
AAAGAACGAT GTTGAAGAG GTATGGTGGT TTGTCAGCCT AACAGCGTGA        600
AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCTTCA GAAAGAAGAA        650
GGCGGACGTC ATAAGCCTTT CTTCAGCGGA TACAGACCTC AGTTCTTCTT        700
CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAACTGAAA        750
TGGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA        800
GTTGCTCTTG AAGAAGGAAT GAGATTTGCA A                            831
```

2) INFORMATION FOR SEQ ID NO: 21

```
   (i) SEQUENCE CHARACTERISTICS:
       (A)    LENGTH: 826 bases
       (B)    TYPE: Nucleic acid
       (C)    STRANDEDNESS: Double
       (D)    TOPOLOGY: Linear
```

14

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Chlamydia psittaci*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

```
TGGAGCGATT CTCGTTGTTT CCGCTACTGA CGGTGCGATG CCTCAGACCA      50
AAGAACATAT TCTTTTGGCG AGACAGGTTG GTGTTCCTTA CATCGTTGTT     100
TTCCTTAACA AAATCGATAT GATTTCTCAA GAAGATGCTG AGCTCGTAGA     150
CTTAGTTGAA ATGGAATTGT CCGAACTTCT AGAAGAAAAA GGTTATAAAG     200
GTTGCCCAAT TATCCGTGGT TCTGCTTTGA AAGCCTTAGA AGGTGATGCA     250
AGCTACGTTG AAAAAATTCG CGAGTTAATG CAAGCAGTGG ATGATAACAT     300
CCCTACTCCA GAGCGTGAAG TTGATAAGCC TTTCTTAATG CCTATCGAAG     350
ACGTATTCTC TATTTCTGGT CGTGGTACTG TGGTCACAGG ACGTATCGAG     400
CGTGGAATCG TTAAAGTGGG TGATAAAGTA CAGATTGTTG GTTTAAGAGA     450
TACTAGAGAG ACAATTGTTA CCGGTGTGGA AATGTTCAGA AAAGAACTTC     500
CAGAAGGTCA AGCAGGGGAA AACGTTGGTT TGCTCCTCAG AGGTATCGGT     550
AAGAATGACG TTGAACGTGG TATGGTTATC TGCCAACCTA ATAGCGTGAA     600
ATCTCACACA CAATTTAAAG GTGCTGTCTA CATTCTACAA AAAGAAGAGG     650
GTGGACGTCA TAAACCTTTC TTTACCGGAT ACAGACCTCA GTTCTTCTTC     700
CGTACAACAG ATGTTACAGG TGTTGTAACT CTCCCAGAAG GTACAGAGAT     750
GGTTATGCCA GGCGATAACG TTGAATTCGA AGTTCAATTA ATTAGCCCAG     800
TAGCTCTAGA AGAAGGTATG AGATTT                               826
```

2) INFORMATION FOR SEQ ID NO: 22

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 822 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Chlamydia trachomatis*
        (B)   STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

```
GGGGCTATTC TAGTAGTTTC TGCAACAGAC GGAGCTATGC CTCAAACTAA      50
AGAGCATATT CTTTTGGCAA GACAAGTTGG GGTTCCTTAC ATCGTTGTTT     100
TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC     150
TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG     200
GTGTCCAATC ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGGGATGCTG     250
CATACATAGA GAAAGTTCGA GAGCTAATGC AAGCCGTCGA TGATAATATC     300
CCTACTCCAG AAAGAGAAAT TGACAAGCCT TTCTTAATGC CCATTGAGGA     350
CGTGTTCTCT ATCTCCGGAC GAGGAACTGT AGTAACTGGA CGTATTGAGC     400
GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT     450
ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTCAGAA AAGAACTCCC     500
AGAAGGTCGT GCAGGAGAGA ATGTTGGATT GCTCCTCAGA GGTATTGGTA     550
AGAACGATGT GGAAAGAGGA ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA     600
CCTCATACAC GGTTTAAGTG TGCTGTTTAC GTTCTGCAAA AAGAAGAAGG     650
TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA TTCTTCTTCC     700
GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG     750
GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAGTTGA TTAGCCCTGT     800
GGCTTTAGAA GAAGGTATGA GA                                   822
```

15

2) INFORMATION FOR SEQ ID NO: 23

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 835 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Chryseobacterium meningosepticum*
        (B)   STRAIN: CDC B7681

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

```
CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAACTA       50
GAGAACACAT CCTACTTTGC CGTCAGGTAA ACGTACCTAG AATTGTTGTG      100
TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAATTGT TAGAGCTTGT      150
TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA      200
ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTTAA CGGTGATGCT      250
AAGTGGGTAG CTACTGTAGA AGCTCTAATG GATGCTGTTG ATACTTGGAT      300
CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCCTTATG CCAATCGAAG      350
ACGTATTCTC TATTACAGGT AGAGGTACTG TAGCAACTGG TAGAATCGAG      400
GCTGGTGTAA TCAACACAGG TGATCCTGTT GACATCGTAG GTATGGGTGA      450
CGAGAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC      500
TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT      550
GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTCAGT      600
TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG      650
AAGGTGGACG TCACACTCCA TTCCACAACA AATACCGTCC TCAGTTCTAT      700
GTAAGAACTA CTGACGTTAC AGGTGAAATC TTCTTACCAG AAGGTGTAGA      750
AATGGTAATG CCTGGTGATA ACTTAACTAT CACTGTAGAA TTGTTACAAC      800
CAATCGCTCT TAACGAGGGT CTTAGATTCG CGATC                      835
```

2) INFORMATION FOR SEQ ID NO: 24

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 816 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Citrobacter amalonaticus*
        (B)   STRAIN: ATCC 25405

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC       50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT      150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG      200
ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
```

SUBSTITUTE SHEET (RULE 26)

```
      GAGTGGGAAG CGAAAATCAT CGAACTGGCC GGCTTCCTGG ATTCTTACAT    300
      CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG    350
      ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA    400
      CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA    450
  5   GACTGCCAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG    500
      ACGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA    550
      CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCWCCATCAA    600
      GCCGCACACC ATGTTCGAAT CYGAAGTGTA CATCCTGTCC AAAGACGAAG    650
      GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC    700
 10   CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTTGAGAT    750
      GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA    800
      TCGCGATGGA CGACGG                                       816
```

15

2) INFORMATION FOR SEQ ID NO: 25

    (i) SEQUENCE CHARACTERISTICS:
20   (A)   LENGTH: 825 bases
         (B)   TYPE: Nucleic acid
         (C)   STRANDEDNESS: Double
         (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA
25

    (vi) ORIGINAL SOURCE:
         (A)   ORGANISM: *Citrobacter braakii*
         (B)   STRAIN: ATCC 43162

30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

```
      CGCGATCCTG GTTGTTGCTG CAACTGACGG CCCGATGCCG CAGACTCGTG    50
      AGCACATCCT GCTGGGTCGY CAGGTAGGCG TTCCGTACAT CATCGTGTTC    100
      CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA    150
 35   AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGATTTCCCG GGCGACGACA    200
      CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAWGCAGAG    250
      TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATCCC    300
      GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCT ATCGAAGACG    350
      TATTCTCCAT CTCTGGTCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC    400
 40   GGTATCATCA AAGTTGGTGA AGAAGTTGAA ATCGTTGGTA TCAARGACAC    450
      TGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG    500
      AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAGCGT    550
      GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCT CTATCAAGCC    600
      GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG    650
 45   GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCGCAGTT CTACTTCCGT    700
      ACTACTGACG TGACTGGTAC CATCGAACTG CCGGAAGGCG TTGAGATGGT    750
      AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG    800
      CGATGGACGA CGGTCTGCGT TTCGC                              825
```

50

2) INFORMATION FOR SEQ ID NO: 26

    (i) SEQUENCE CHARACTERISTICS:
55   (A)   LENGTH: 830 bases
         (B)   TYPE: Nucleic acid
         (C)   STRANDEDNESS: Double
         (D)   TOPOLOGY: Linear

60   (ii) MOLECULE TYPE: Genomic DNA

17

```
    (vi) ORIGINAL SOURCE:
         (A)    ORGANISM: Citrobacter koseri
         (B)    STRAIN: ATCC 27156

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

    CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC    50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG   100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT   150
    TGAGATGGAA GTGCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG   200
    ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAMGCT   250
    GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT   300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG   350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG   400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATYGTTG GTATCAAAGA   450
    GACTGCGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG   500
    ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA   550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GYTCCATCAA   600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATYCTGTCY AAAGATGAAG   650
    GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC   700
    CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT   750
    GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA   800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA                         830


2) INFORMATION FOR SEQ ID NO: 27

    (i) SEQUENCE CHARACTERISTICS:
         (A)    LENGTH: 827 bases
         (B)    TYPE: Nucleic acid
         (C)    STRANDEDNESS: Double
         (D)    TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
         (A)    ORGANISM: Citrobacter farmeri
         (B)    STRAIN: ATCC 51112

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

    CGCGATCCTG GTTGTTGCTG CGACTGACGG CCCGATGCCG CAGACTCGTG    50
    AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTC   100
    CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA   150
    GATGGAAGTT CGTGAACTGC TGTCTCAGTA CGATTTCCCG GGCGACGACA   200
    CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG   250
    TGGGAAGCGA AAATCATCGA ACTGGCAGGC TTCCTGGATT CTTACATCCC   300
    GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG   350
    TATTCTCCAT CTCTGGTCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC   400
    GGTATCATCA AAGTGGGTGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC   450
    TGCCAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG   500
    AAGGCCGTGC TGGTGAGAAC GTAGGTGTTC TGCTGCGTGG TATCAAACGT   550
    GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCW CCATCAAGCC   600
    RCACACTATG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG   650
    GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT   700
    ACGACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGTG TTGAGATGGT   750
    TATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG   800
    CGATGGACGA CGGTCTGCGT TTCGCAA                            827
```

18

2) INFORMATION FOR SEQ ID NO: 28

    (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 797 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
      (A)   ORGANISM: *Citrobacter freundii*
      (B)   STRAIN: ATCC 8090

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

```
CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA        50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC       100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TAGAAATGGA       150
AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACTCCGA       200
TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGAAGC AGAGTGGGAA       250
GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCAGAACC       300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCTATCGAA GACGTATTCT       350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC       400
ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTGCTAA       450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC       500
GTGCTGGTGA GAACGTTGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA       550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCTCTATCA AGCCGCACAC       600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGACGAA GGCGGCCGTC       650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT       700
GACGTGACTG GTACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC       750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCGA         797
```

2) INFORMATION FOR SEQ ID NO: 29

    (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 826 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
      (A)   ORGANISM: *Citrobacter sedlakii*
      (B)   STRAIN: ATCC 51115

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

```
CGGCGCGATC CTGGTTGTTG CCGCGACTGA CGGCCCGATG CCGCAGACCC        50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG       100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT       150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG       200
ACACGCCGAT CGTTCGTGG TCAGCTCTGA AAGCGCTGGA AGGCGACGCA       250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT       300
```

19

```
     TCCGGAACCA  GAGCGTGCGA  TTGACAAGCC  GTTCCTGCTG  CCGATCGAAG       350
     ACGTATTCTC  CATCTCCGGT  CGTGGTACCG  TTGTTACCGG  TCGTGTAGAG       400
     CGCGGTATCA  TCAAAGTGGG  CGAAGAAGTT  GAAATCGTTG  GTATCAAAGA       450
     GACTGCGAAG  TCTACCTGTA  CTGGCGTTGA  AATGTTCCGC  AAACTGCTGG       500
  5  ACGAAGGCCG  TGCGGGTGAG  AACGTAGGTG  TTCTGCTGCG  TGGTATCAAA       550
     CGTGAAGAAA  TCGAACGTGG  TCAGGTACTG  GCGAAGCCGG  GCACCATCAA       600
     GCCGCACACC  AAGTTCGAAT  CTGAAGTGTA  TATTCTGTCC  AAAGATGAAG       650
     GCGGCCGTCA  TACTCCGTTC  TTCAAAGGCT  ACCGTCCGCA  GTTCTACTTC       700
     CGTACAACTG  ACGTGACTGG  CACCATCGAA  CTGCCGGAAG  GCGTAGAGAT       750
 10  GGTAATGCCG  GGCGACAACA  TCAAAATGGT  TGTTACCCTG  ATCCACCCGA       800
     TCGCGATGGA  CGACGGTCTG  CGTTTC                                   826
```

```
     GCGATCCTGG  TTGTTGCTGC  GACTGACGGC  CCGATGCCGC  AGACTCGTGA        50
     GCACATCCTG  CTGGGTCGTC  AGGTAGGCGT  TCCGTACATC  ATCGTGTTCC       100
     TGAACAAATG  CGACATGGTT  GATGACGAAG  AGCTGCTGGA  ACTGGTAGAA       150
     ATGGAAGTTC  GTGAACTTCT  GTCTCAGTAC  GATTTCCCGG  GCGACGACAC       200
 35  TCCGATCGTT  CGTGGTTCTG  CTCTGAAAGC  GCTGGAAGGC  GAAGCAGAGT       250
     GGGAAGCGAA  AATCATCGAA  CTGGCTGGCT  TTCTGGATTC  TTACATCCCG       300
     GAACCAGAGC  GTGCGATTGA  CAAGCCGTTC  CTGCTRCCTA  TCGAAGACGT       350
     ATTCTCCATC  TCCGGTCGTG  GTACCGTTGT  TACCGGTCGT  GTAGAGCGCG       400
     GTATCATCAA  AGTTGGTGAA  GAAGTTGAAA  TCGTTGGTAT  CAAAGACACC       450
 40  GCTAAGTCTA  CCTGTACCGG  CGTTGAAATG  TTCCGCAAAC  TGCTGGACGA       500
     AGGCCGTGCT  GGTGAGAACG  TTGGTGTTCT  GCTGCGTGGT  ATCAAACGTG       550
     AAGAAATCGA  ACGTGGTCAG  GTACTGGCTA  AGCCGGGCTC  TATCAAGCCG       600
     CACACCAAGT  TCGAATCTGA  AGTGTACATC  CTGTCCAAAG  ACGAAGGCGG       650
     CCGTCATACT  CCGTTCTTCA  AAGGCTACCG  TCCGCAGTTC  TACTTCCGTA       700
 45  CTACTGACGT  GACTGGTACC  ATCGAACTGC  CGGAAGGCGT  AGAGATGGTA       750
     ATGCCGGGCG  ACAACATYAA  AATGGTTGTT  ACYCTGATCC  ACCCGATCGC       800
     GATGGACGAC  GGTCTGCGTT  TCG                                      823
```

```
        (vi) ORIGINAL SOURCE:
             (A)    ORGANISM: Citrobacter youngae
             (B)    STRAIN: ATCC 29935

5       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

        GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG      50
        TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
        TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTA     150
10      GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC CGGGCGACGA     200
        TACGCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGAAGCAG     250
        AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC     300
        CCGGAACCAG AACGTGCTAT CGATAAGCCG TTCCTGCTGC CAATCGAAGA     350
        CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACTGGT CGTGTAGAAC     400
15      GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG     450
        ACTGCCAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
        CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
        GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCTATCAAG     600
        CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
20      CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     700
        GTACTACTGA CGTGACGGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG     750
        GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT     800
        CGCGATGGAT GACGGTCTGC GTTTCG                               826

25


        2) INFORMATION FOR SEQ ID NO: 32

        (i) SEQUENCE CHARACTERISTICS:
30          (A)    LENGTH: 841 bases
            (B)    TYPE: Nucleic acid
            (C)    STRANDEDNESS: Double
            (D)    TOPOLOGY: Linear

35      (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
             (A)    ORGANISM: Clostridium perfringens
             (B)    STRAIN: ATCC 13124
40
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

        CGGAGCTATA TTAGTTTGTT CAGCAGCTGA TGGTCCAATG CCTCAAACAA      50
        GAGAGCACAT CTTATTATCA TCAAGAGTTG GAGTTGACCA CATCGTAGTA     100
45      TTCTTAAACA AAGCAGATAT GGTTGACGAC GAAGAATTAT TAGAATTAGT     150
        TGAAATGGAA GTTAGAGAGT TATTAAGCGA GTACAACTTC CCAGGAGACG     200
        AYATTCCAGT AATCAARGGA TCAGCTTTAG TAGCATTAGA AAACCCAACT     250
        GACGAAGCTG CAACAGCTTG TATCAGAGAG TTAATGGATG CTGTAGATAG     300
        CTACATCCCA ACACCAGAAA GAGCAACAGA TAAGCCATTC TTAATGCCAG     350
50      TAGAGGACGT ATTCACAATC ACTGGTAGAG GAACAGTTGC AACAGGAAGA     400
        GTTGAAAGAG GAGTTCTACA TGTAGGAGAC GAAGTAGAAG TAATCGGATT     450
        AACTGAAGAA AGAAGAAAAA CTGTTGTAAC AGGAATCGAA ATGTTCAGAA     500
        AGTTATTAGA TGAAGCACAA GCTGGAGATA ACATCGGAGC ATTATTAAGA     550
        GGTATCCAAA GAACTGAYAT CGAAAGAGGT CAAGTTTTAG CTCAAGTTGG     600
55      AACAATCAAC CCACACAAAA AATTCGTAGG TCAAGTATAC GTACTTAAAA     650
        AAGAAGAAGG TGGAAGACAT ACTCCATTCT TCGATGGATA CAGACCACAA     700
        TTCTACTTCA GAACAACAGA CGTTACAGGA TCAATCAAAT TACCAGAAGG     750
        AATGGAAATG GTTATGCCTG GAGACCACAT CGACATGGAA GTTGAATTAA     800
        TCACAGAAAT CGCTATGGAY GAAGGATTAA GATTCGCTAT C              841
60
```

2) INFORMATION FOR SEQ ID NO: 33

    5   (i) SEQUENCE CHARACTERISTICS:
                  (A)   LENGTH: 822 bases
                  (B)   TYPE: Nucleic acid
                  (C)   STRANDEDNESS: Double
                  (D)   TOPOLOGY: Linear
   10
               (ii) MOLECULE TYPE: Genomic DNA

               (vi) ORIGINAL SOURCE:
                  (A)   ORGANISM: *Comamonas acidovorans*
   15   (B)   STRAIN: ATCC 15668

               (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

           CGGCGCCATC CTGGTGTGCT CGGCCGCTGA CGGCCCCATG CCCCAGACCC   50
   20   GCGAGCACAT CCTGCTGGCC CGTCAGGTGG GCGTGCCCTA CATCATCGTG   100
           TTCCTGAACA AGTGCGACAT GGTGGACGAC GAAGAGCTGC TGGAACTGGT   150
           CGAAATGGAA GTGCGCGAGC TGCTTGCCAA GTACGACTTC CCCGGCGACG   200
           ACACCCCCAT CATCCGCGGC TCGGCCAAGC TGGCCCTGGA AGGCGACCAG   250
           TCCGACAAGG GCGAACCTGC CATCCTGCGC CTGGCTGAAG CACTGGACTC   300
   25   CTACATCCCC ACGCCCGAGC GCGCTGTGGA CGGCGCCTTT GCAATGCCCG   350
           TGGAAGACGT GTTCTCGATC TCTGGCCGTG GCACCGTGGT GACTGGCCGT   400
           ATCGAGCGCG GCATCATCAA GGTCGGCGAA GAAATCGAAA TCGTCGGTAT   450
           CCGCGACACC CAGAAGACCA TCGTCACCGG CGTGGAAATG TTCCGCAAGC   500
           TGCTGGACCA AGGTCAAGCT GGCGACAACG TGGGTCTGCT GCTGCGCGGC   550
   30   ACCAAGCGTG AAGACGTGGA ACGCGGCCAA GTGCTGTGCA AGCCCGGCTC   600
           CATCAAGCCC CACACCCACT TCACGGCTGA GGTGTACGTG CTGTCCAAGG   650
           ACGAAGGTGG TCGCCACACT CCGTTCTTCA ACAACTACCG TCCCCAGTTC   700
           TATTTCCGTA CGACCGACGT GACCGGCTCC ATCGAGCTGC CCGCCGACAA   750
           GGAAATGGTG ATGCCTGGCG ACAACGTGTC GATCACCGTC AAGCTGATCG   800
   35   CCCCCATCGC CATGGAAGAA GG   822

           2) INFORMATION FOR SEQ ID NO: 34
   40
               (i) SEQUENCE CHARACTERISTICS:
                  (A)   LENGTH: 702 bases
                  (B)   TYPE: Nucleic acid
                  (C)   STRANDEDNESS: Double
   45   (D)   TOPOLOGY: Linear

               (ii) MOLECULE TYPE: Genomic DNA

               (vi) ORIGINAL SOURCE:
   50   (A)   ORGANISM: *Corynebacterium bovis*
                  (B)   STRAIN: ATCC 7715

               (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

   55   GCCGCAGACC CGTGAGCACG TCCTCCTGGC CCGTCAGGTC GGTGTGCCCT   50
           ACATCCTCGT CGCCCTCAAC AAGTGCGACA TGGTCGACGA CGAGGACCTC   100
           ATCGAGCTCG TCGAGATGGA GGTCCGTGAG CTCCTCGCCG AGCAGGACTA   150
           CGACGAGGAC GCCCCGATCA TCCACATCTC CGCCCTCAAG GCCCTCGAGG   200
           GTGACCCGGA GTGGACGCAG CGCATCGTCG ACCTCATGAA GGCCTGCGAC   250
   60   GACGCCATCC CGGATCCGGA GCGCGAGACG GACAAGCCGT TCCTCATGCC   300

                                     22

```
    GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC          350
    GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT          400
    ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA          450
    CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC          500
 5  GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG          550
    GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC          600
    CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTCGACAAC TACCGTCCGC          650
    AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG          700
    GG                                                             702
10
```

2) INFORMATION FOR SEQ ID NO: 35

15   (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 689 bases
            (B)   TYPE: Nucleic acid
            (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear
20
         (ii) MOLECULE TYPE: Genomic DNA

         (vi) ORIGINAL SOURCE:
            (A)   ORGANISM: *Corynebacterium cervicis*
25   (B)   STRAIN: NCTC 10604

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

```
    GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GGCGTTCCGA          50
30  CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG          100
    CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT          150
    CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG          200
    GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC          250
    ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC          300
35  GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC          350
    GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT          400
    ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA          450
    GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG          500
    GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT          550
40  TCGATCACCC CGCACACCAA CTTCACCGGA CAGGTCTACA TCCTCAAGAA          600
    GGAAGAAGGC GGTCGTCACA ACCCGTTCTT CTCGAACTAC CGTCCGCAGT          650
    TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC                      689
```

45
   2) INFORMATION FOR SEQ ID NO: 36

         (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 804 bases
50   (B)   TYPE: Nucleic acid
            (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

         (ii) MOLECULE TYPE: Genomic DNA
55
         (vi) ORIGINAL SOURCE:
            (A)   ORGANISM: *Corynebacterium flavescens*
            (B)   STRAIN: ATCC 10340

60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

                                23

```
      GGTTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTC        50
      TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG       100
      TGCGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT       150
  5   CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC       200
      ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC       250
      ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG       300
      CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA       350
      CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG       400
 10   GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAGT CCATCTCCAC       450
      CACCGTTACC GGTATCGAAA TGTTCCGCAA GATGATGGAC TACACCGAGG       500
      CTGGCGACAA CTGTGGTCTG CTTCTGCGTG GTACCAAGCG TGAAGAGGTC       550
      GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA       600
      GTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA       650
 15   CCCCGTTCAT GGACAACTAC CGTCCGCAGT TCTACTTCCG TACCACTGAC       700
      GTGACCGGCG TTGTTCACCT GCCTGAGGGC ACCGAGATGG TCATGCCTGG       750
      CGACAACGTT GATATGACCG TTGAGCTCAT CCAGCCCGTC GCTAGGATGA       800
      GGGC                                                        804
```

 20

     2) INFORMATION FOR SEQ ID NO: 37

        (i) SEQUENCE CHARACTERISTICS:
 25   (A)   LENGTH: 692 bases
           (B)   TYPE: Nucleic acid
           (C)   STRANDEDNESS: Double
           (D)   TOPOLOGY: Linear

 30   (ii) MOLECULE TYPE: Genomic DNA

       (vi) ORIGINAL SOURCE:
           (A)   ORGANISM: *Corynebacterium kutscheri*
           (B)   STRAIN: ATCC 15677
 35
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```
      TGCCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCT        50
      TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT       100
 40   CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT       150
      ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG       200
      GGCGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTGA       250
      TGACTCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC       300
      CTATCGAGGA TATCTTCACC ATCACCGGTC GTGGCACCGT TGTTACCGGT       350
 45   CGTGTTGAGC GCGGTTCCTT GAAGGTGAAT GAGGACGTCG AGATCATCGG       400
      CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC       450
      GTAAGCTTCT TGATTACACC GAAGCTGGCG ATAACTGTGG TCTGCTTCTT       500
      CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTCAGGTTG TTGTTAAGCC       550
      AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT       600
 50   CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA       650
      CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG              692
```

 55   2) INFORMATION FOR SEQ ID NO: 38

        (i) SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 797 bases
           (B)   TYPE: Nucleic acid
 60   (C)   STRANDEDNESS: Double

                                    24

     (D)   TOPOLOGY: Linear

    (ii)MOLECULE TYPE: Genomic DNA

5   (vi)ORIGINAL SOURCE:
       (A)   ORGANISM: *Corynebacterium minutissimum*
       (B)   STRAIN: ATCC 23348

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 38
10

```
CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG    50
TTCTTCTGGC CCGCCAGGTT GGCGTTCCGT ACATCCTCGT TGCACTGAAC   100
AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA   150
GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG   200
TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG   250
TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA   300
GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA   350
TTACCGGCCG CGGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG   400
AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC   450
CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG   500
AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG   550
GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GGCGCTTACA CCCCGCACAC   600
CAAGTTCGAG GGTTCCGTCT ACGTCCTGAA GAAGGAAGAG GGCGGCCGCC   650
ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC   700
GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC   750
GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA      797
```

30   2)INFORMATION FOR SEQ ID NO: 39

      (i)SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 702 bases
       (B)   TYPE: Nucleic acid
35   (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii)MOLECULE TYPE: Genomic DNA

40   (vi)ORIGINAL SOURCE:
       (A)   ORGANISM: *Corynebacterium mycetoides*
     (B)   STRAIN: ATCC 21134

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 39
45

```
GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT    50
ACATCCTCGT TGCGCTGAAC AAGTGCGACA TGGTTGATGA TGAGGAGATC   100
ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA   150
CGACGAGGAC GCCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG   200
GCGACGAGAA GTGGGTTCAG TCCGTGCTCG ACCTCATGCA GGCGTGCGAC   250
GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC   300
GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC   350
GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACGAGGTCGA GATCATCGGC   400
ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA   450
CAAGCTGCTC GATACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC   500
GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG   550
GGCGCCTACA CCCCGCACAC CAAGTTCGAG GGTTCCGTCT ACGTCCTGTC   600
CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC   650
AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG   700
60  GG                                                    702
```

2) INFORMATION FOR SEQ ID NO: 40

     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 674 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Corynebacterium pseudogenitalium*
        (B)   STRAIN: ATCC 33038

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

```
GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGCGCTGA ACAAGTGCGA      50
CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG     100
AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC     150
TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT     200
TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA     250
CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC     300
CGCGGTACCG TTGTTACCGG CCGTGTTGAG CGTGGCCGTC TGAACGTCAA     350
CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG     400
TTACCGGTAT CGAGATGTTC CGCAAGATGA TGGACTACAC CGAGGCTGGC     450
GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG     500
TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCG     550
AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG     600
TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC     650
CGGTGTTGTT CACCTGCCAG AGGG                                674
```

2) INFORMATION FOR SEQ ID NO: 41

     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 694 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Corynebacterium renale*
        (B)   STRAIN: ATCC 19412

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

```
TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT      50
TACATCCTCG TTGCACTGAA CAAGTGCGAC ATGGTCGACG ACGAAGAAAT     100
CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT     150
ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC     200
GGCGAGCAGA AGTGGGTTGA CTCCATCGTC GAACTGATGG AAGCTTGCGA     250
CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC     300
CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC     350
CGTGTCGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG     400
```

```
        TATCAAGGAC AAGTCCCAGA AGACCACCGT CACCGGTATC GAGATGTTCC        450
        GCAAGATGCT GGACTACACC GAAGCTGGCG ACAACTGTGG TCTGCTGCTC        500
        CGCGGCATCG GCCGTGAGGA TGTCGAGCGT GGCCAGGTTA TCATCAAGCC        550
        AGGCGCTTAC ACCCCTCACT CTGAGTTCGA GGGCTCTGTC TACGTCCTGT        600
     5  CCAAGGACGA GGGTGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA        650
        CAGTTCTACT TCCGCACCAC CGACGTGACC GGCGTTGTGC ACCT            694
```

10　2)INFORMATION FOR SEQ ID NO: 42

　　　　(i)SEQUENCE CHARACTERISTICS:
　　　　　　(A)　　LENGTH: 687 bases
　　　　　　(B)　　TYPE: Nucleic acid
15　　　　　(C)　　STRANDEDNESS: Double
　　　　　　(D)　　TOPOLOGY: Linear

　　　(ii)MOLECULE TYPE: Genomic DNA

20　(vi)ORIGINAL SOURCE:
　　　　　　(A)　　ORGANISM: *Corynebacterium ulcerans*
　　　　　　(B)　　STRAIN: NCTC 8665

　　　(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 42
25
```
        GCCGCAGACC CGCGAGCACG TTCTGCTGGC TCGCCAGGTT GGCGTTCCKT        50
        ACATCCTSGT TGCACTGAAC AAGTGCGACA TGGTTGACGA TGAGGARCTC        100
        CTSGAGCTCG TCGAGATGGA GGTCCGCGAG CTGCTGGCTG AGCAGGACTA        150
        CGACGAGGAA GCTCCGRTCG TTCACATCTC CGCWCTGAAC GCCCTGGACG        200
     30 GCGACSAGAA GTGGGCTVAC TCCATCCTCG AGCTGATGCA GGCTTGCGAC        250
        GAGTCCATCC CGGATCCGGA GCGCGAGACC GACAAGCCGT TCCTGATGCC        300
        GATTGAGGAC ATCTTCACCA TTACCGGTCG CGGYACCGTT GTTACCGGCC        350
        GTGTTGAGCG TGGCDTCCTG AACGTSAACG ACGASGTTGA GATCATGGGY        400
        ATCCGGGAGA AGTCCCAGAA GACCACCGTY ACCKSCATCG AGATGTTCAA        450
     35 CAAGMTGMTG GACWCCGCAG AGGCTGGCGA CAACGCTGSW CTGCTGCTGC        500
        GTGGTMTSAA GCGTGAGGAC GTTGAGCGTG GCCAGATCAT CGYTAAGCCG        550
        GGCGCKTACA CCCCGCACAC CGAGTTCGAG GGCTCCGTCT ACGTCCTGTC        600
        CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC        650
        AGTTCTACTT CCGCACCACC GACGTSACCG GTGTTGT                   687
     40
```

　　　2)INFORMATION FOR SEQ ID NO: 43

45　　　(i)SEQUENCE CHARACTERISTICS:
　　　　　　(A)　　LENGTH: 778 bases
　　　　　　(B)　　TYPE: Nucleic acid
　　　　　　(C)　　STRANDEDNESS: Double
　　　　　　(D)　　TOPOLOGY: Linear
50
　　　(ii)MOLECULE TYPE: Genomic DNA

　　　(vi)ORIGINAL SOURCE:
　　　　　　(A)　　ORGANISM: *Corynebacterium urealyticum*
55　　　　　(B)　　STRAIN: ATCC 43042

　　　(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 43

```
        CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT        50
     60 TCTGCTGGCT CGCCAGGTTG GCGTTCCGTA CATCCTCGTT GCACTGAACA        100
```

27

```
        AGTGCGACAT  GGTTGACGAT  GAGGAGCTCC  TCGAGCTCGT  CGAGATGGAG      150
        GTCCGCGAGC  TTCTGGCTGA  GCAGGACTAC  GACGAGGAGG  CTCCGGTCGT      200
        CCCGATCTCC  GCACTGGGCG  CCCTGGACGG  CGATCAGAAG  TGGGTCGACT      250
        CCATCCTCGA  GCTCATGAAG  GCTTGCGACG  AGTCCATCCC  GGACCCGGAG      300
   5    CGCGAGACCG  ACAAGCCGTT  CCTGATGCCG  GTTGAGGACA  TCTTCACCAT      350
        TACCGGTCGC  GGCACCGTCG  TTACCGGCCG  TGTTGAGCGT  GGCGTCCTGA      400
        ACCTGAACGA  CGAGGTCGAG  ATCCTGGGCA  TCCGCGAGAA  GTCCACCAAG      450
        ACCACCGTCA  CCTCCATCGA  GATGTTCAAC  AAGCTGCTGG  ACACCGCAGA      500
        GGCTGGCGAC  AACGCTGCAC  TGCTGCTGCG  TGGTCTGAAG  CGTGAGGACG      550
   10   TCGAGCGAGG  CCAGATCATC  GCTAAGCCGG  GCGCTTACAC  CCCGCACACC      600
        GAGTTCGAGG  GCTCCGTCTA  CGTCCTGTCC  AAGGACGAGG  GCGGCCGTCA      650
        CACCCCGTTC  TTCGACAACT  ACCGTCCGCA  GTTCTACTTC  CGTACCACCG      700
        ACGTCACCGG  TGTCGTTACC  CTGCCAGAGG  GCACCGACAT  GGTCATGCCG      750
        GGCGACAACG  TTGAGATGAG  CGTCAAGC                                778
   15
```


   2) INFORMATION FOR SEQ ID NO: 44

   20   (i) SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 703 bases
                (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear
   25
           (ii) MOLECULE TYPE: Genomic DNA

           (vi) ORIGINAL SOURCE:
                (A)   ORGANISM: *Corynebacterium xerosis*
   30   (B)   STRAIN: ATCC 373

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

```
        CGCAGACCCG  TGAGCACGTC  CTCCTGGCCC  GCCAGGTCGG  CGTCCCCTAC       50
   35   ATCCTCGTCG  CCCTGAACAA  GTGCGACATG  GTCGACGATG  AGGAGATCAT      100
        CGAGCTCGTG  GAGATGGAGG  TGCGTGAGCT  TCTCGCCGAG  CAGGACTACG      150
        ACGAGGAGGC  CCCGATCGTG  CACATCTCCG  CCCTGGGCGC  CCTCAATGGC      200
        GAAGAGAAGT  GGGTCGACTC  CATCGTCGAG  CTCATGAACG  CCGTCGACGA      250
        GAACGTTCCG  GACCCGGTCC  GCGAGACCGA  CAAGCCGTTC  CTGATGCCCG      300
   40   TCGAGGACAT  CTTCACCATC  ACCGGCCGCG  GCACCGTCGC  CACCGGTCGC      350
        GTGGAGCGCG  GCACCCTGAA  GGTCAACGAC  GAGGTCGAGA  TCCTGGGCAT      400
        CCAGGAGAAG  TCCCAGACCA  CCACCGTCAC  CGGCATCGAG  ATGTTCCGCA      450
        AGCTGCTGGA  CTCCGCCGAG  GCCGGCGACA  ACTGTGGCCT  GCTGCTCCGC      500
        GGCATCAAGC  GCGAGGACAT  CGAGCGCGGC  CAGATCATCG  CGAAGCCGGG      550
   45   CGCCTACACC  CCGCACACCG  AGTTCGAGGG  CTCCGTCTAC  ATCCTGGCCA      600
        AGGACGAGGG  CGGCCGCCAC  ACCCCGTTCT  TCGACAACTA  CCGTCCGCAG      650
        TTCTACTTCC  GCACCACCGA  CGTCACCGGC  GTCGTGAAGC  TGCCGGAGGG      700
        CAC                                                            703
```

   50

   2) INFORMATION FOR SEQ ID NO: 45

           (i) SEQUENCE CHARACTERISTICS:
   55   (A)   LENGTH: 832 bases
                (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

   60   (ii) MOLECULE TYPE: Genomic DNA

                                    28

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Coxiella burnetii*
    (B)   STRAIN: Nine Mile phase II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

```
GGAGCGATAT TGGTGGTGAG CGCAGCGGAC GGCCCGATGC CGCAAACGCG        50
GGAACACATT GTATTGGCGA AGCAAGTGGG TGTTCCGAAC ATAGTGGTTT       100
ACTTGAACAA AGCGGACATG GTGGATGACA AAGAGCTGTT GGAATTAGTG       150
GAAATGGAAG TGAGGGATTT ATTGAACAGT TATGATTTCC CTGGGGATGA       200
GACGCCGATA ATAGTGGGGT CAGCGTTAAA GGCGTTAGAA GGTGACAAGA       250
GTGAGGTTGG GGAGCCATCG ATAATCAAAT TAGTGGAAAC GATGGACACG       300
TACTTCCCGC AGCCGGAGCG AGCGATAGAC AAACCGTTTT TAATGCCGAT       350
CGAAGATGTG TTTTCGATAT CGGGCCGAGG GACGGTGGTG ACGGGACGCG       400
TAGAGCGAGG GATCATCAAA GTGGGCGACG AGATAGAGAT TGTGGGGATC       450
AAGGACACGA CGAAGACGAC GTGCACGGGC GTTGAGATGT TTCGCAAATT       500
ATTGGATGAA GGTCAAGCGG GTGACAACGT AGGAATTTTA TTGAGAGGGA       550
CGAAACGCGA AGAAGTGGAG CGTGGTCAAG TATTGGCGAA ACCGGGATCG       600
ATCACGCCAC ACAAGAAATT TGAGGCGGAG ATTTATGTGT TGTCGAAGGA       650
AGAAGGGGGA CGCCACACAC CGTTTTTACA AGGCTATCGA CCGCAATTTT       700
ATTTCCGCAC GACGGACGTG ACGGGCCAGT TATTGAGTTT ACCGGAGGGG       750
ATAGAGATGG TGATGCCGGG AGATAACGTG AAAGTGACGG TTGAATTGAT       800
TGCGCCGGTA GCGATGGATG AAGGGCTACG AT                          832
```

2) INFORMATION FOR SEQ ID NO: 46

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 816 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Edwardsiella hoshinae*
        (B)   STRAIN: ATCC 33379

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

```
GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG        50
TGAGCACATC CTGCTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT       100
TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT       150
GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA       200
TACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG       250
AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACGCTGGA CTCCTACATT       300
CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA       350
CGTATTCTCA ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC       400
GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTAGG TATCAAGCCG       450
ACCACCAAGA CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA       500
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTACCAAGC       550
GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT       600
CCGCACACCA AGTTCGAATC AGAAGTGTAC ATCCTGAGCA AGGATGAAGG       650
CGGCCGTCAT ACTCCGTTCT TCAAAGGTTA CCGTCCGCAG TTCTACTTCC       700
GTACCACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG       750
GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT       800
CGCCATGGAC GATGGT                                           816
```

29

2) INFORMATION FOR SEQ ID NO: 47

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 821 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Edwardsiella tarda*
        (B)   STRAIN: ATCC 15947

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

```
GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG    50
TGAGCACATC CTGTTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT   100
TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT   150
GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA   200
CACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG   250
AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACTCTGGA CTCCTACATC   300
CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA   350
CGTATTCTCT ATCTCTGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC   400
GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTTGG TATCAAGCCG   450
ACCACCAAGA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA   500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAGC   550
GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT   600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGAGCA AGGATGAAGG   650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC   700
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG   750
GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT   800
CGCCATGGAC GATGGTCTGC G                                  821
```

2) INFORMATION FOR SEQ ID NO: 48

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 830 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Eikenella corrodens*
        (B)   STRAIN: ATCC 23834

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

```
CGGTGCCATC CTGGTGGTAT CCGCTGCTGA CGGCCCCATG CCTCAGACTC    50
GCGAACACAT CCTGTTGGCT CGTCAGGTAG GTGTACCCTA CATCCTCGTA   100
TTCATGAACA AATGCGACAT GGTAGATGAT GCCGAGCTGC TTGAGTTGGT   150
TGAGATGGAA ATCCGCGACC TGCTCTCCAG CTATGACTTC CCTGGTGACG   200
ACTGCCCGAT CGTACAAGGT TCCGCTCTCA AAGCCCTCGA AGGCGATGCC   250
```

30

```
      GGTTACAAAG AAAAAATCTT CGAACTAGCT GCTGCTTTGG ATAGCTACAT      300
      CCCCACTCCT CAACGTGCTG TAGACAAACC CTTCCTGTTG CCGATCGAAG      350
      ACGTATTCTC TATCTCCGGC CGTGGTACCG TAGTAACCGG TCGTGTAGAG      400
      CGCGGCATCA TCAAAGTAGG TGAAGAGATC GAAATCGTTG GTCTGAAGCC      450
  5   CACTCAGAAA ACTACCTGTA CTGGCGTGGA AATGTTCCGC AAACTGCTGG      500
      ACGAAGGTCA GGCCGGTGAC AACGTAGGCG TACTGCTGCG CGGTACCAAA      550
      CGTGAAGAAG TTGAGCGTGG TCAAGTATTG GCTAAACCCG GCACCATCAC      600
      TCCGCACACC AAGTTCAAAG CCGAAGTATA CGTATTGAGC AAAGAAGAAG      650
      GTGGTCGTCA CACCCCGTTC TTTGCCAACT ACCGTCCACA GTTCTACTTC      700
  10  CGTACTACTG ACGTAACCGG TGCTGTAGAG CTGGAGCCTG GTGTAGAAAT      750
      GGTTATGCCT GGTGAGAACG TAACCATCAC CGTAGAACTG ATTGCTCCGA      800
      TTGCTATGGA AGAAGGTCTG CGCTTTGCGA                           830
```

15

2) INFORMATION FOR SEQ ID NO: 49

    (i) SEQUENCE CHARACTERISTICS:
20
        (A)   LENGTH: 808 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA
25
    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Enterobacter aerogenes*
        (B)   STRAIN: ATCC 13048

30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

```
      GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG       50
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
      TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT      150
  35  GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA      200
      CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG      250
      AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC      300
      CCRGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA      350
      CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
  40  GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAC      450
      ACCGCGAAAA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCTGGTGAGA ACGTAGGYGT TCTGCTGCGT GGTATCAAAC      550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CAGCATCAAG      600
      CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG      650
  45  CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
      GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGRTG      750
      GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
      CGCGATGG                                                    808
```

50

2) INFORMATION FOR SEQ ID NO: 50

    (i) SEQUENCE CHARACTERISTICS:
55
        (A)   LENGTH: 828 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

60   (ii) MOLECULE TYPE: Genomic DNA

31

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Enterobacter agglomerans*
    (B)   STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

```
CGGCGCGATC  CTGGTTGTTG  CTGCGACTGA  CGGCCCGATG  CCGCAGACTC       50
GTGAGCACAT  CCTGCTGGGT  CGTCAGGTAG  GCGTTCCGTA  CATCATCGTG      100
TTCCTGAACA  AATGTGACAT  GGTTGATGAC  GAAGAGCTGC  TGGAACTGGT      150
TGAAATGGAA  GTTCGTGAAC  TTCTGTCTCA  GTACGATTTC  CCGGGCGACG      200
ATACTCCGAT  CGTTCGTGGT  TCTGCTCTGA  AAGCGCTGGA  AGGCGAMGCW      250
GAGTGGGAAG  CGAAAATCAT  CGARCTGGCT  GGCCACCTGG  ATACCTATAT      300
CCCGGAACCA  GAGCGTGCGA  TTGACAAGCC  GTTCCTGCTG  CCGATCGAAG      350
ACGTATTCTC  CATCTCCGGT  CGCGGTACCG  TTGTTACCGG  TCGTGTAGAG      400
CGCGGTATCA  TYAAAGTGGG  CGAAGAAGTT  GAAATCGTTG  GTATCAAAGA      450
TACYGCGAAA  TCAACCTGTA  CCGGCGTTGA  AATGTTCCGC  AAACTGCTGG      500
ACGAAGGCCG  TGCTGGTGAG  AACGTTGGTG  TTCTGCTGCG  TGGTATCAAA      550
CGTGAAGAAA  TCGAACGTGG  TCAGGTACTG  GCTAAGCCGG  GCACCATCAA      600
GCCGCACACC  AAGTTCGAAT  CTGAAGTGTA  CATTCTGTCC  AAAGATGAAG      650
GCGGTCGTCA  CACTCCGTTC  TTCAAAGGCT  ACCGTCCSCA  GTTCTACTTC      700
CGTACAACTG  ACGTGACTGG  CACCATCGAA  CTGCCGGAAG  GCGTAGAGAT      750
GGTAATGCCG  GGCGACAACA  TCAAAATGGT  TGTTACCCTG  ATCCACCCGA      800
TCGCGATGGA  CGACGGTCTG  CGTTCGCA                                828
```

2) INFORMATION FOR SEQ ID NO: 51

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 825 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Enterobacter amnigenus*
        (B)   STRAIN: ATCC 33072

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

```
TGGCGCGATC  CTGGTTGTTG  CTGCAACTGA  TGGCCCTATG  CCACAGACGC       50
GTGAGCACAT  CCTGCTGGGT  CGTCAGGTAG  GCGTTCCTTA  CATCATCGTG      100
TTCCTGAACA  AATGCGACAT  GGTTGATGAC  GAAGAGCTGC  TGGAACTGGT      150
AGAAATGGAA  GTTCGTGAAC  TTCTGTCTCA  GTACGATTTC  CCAGGTGATG      200
ACACTCCAAT  CATCCGTGGT  TCTGCTCTGA  AAGCGCTGGA  AGGCGAAGCA      250
GAGTGGGAAG  CTAAAATCGT  TGAGCTGGCT  GGCTACCTGG  ATTCTTACAT      300
CCCGGAACCA  GAACGTGCTA  TCGATAAGCC  ATTCCTGCTG  CCAATCGAAG      350
ACGTATTCTC  TATCTCCGGC  CGTGGTACTG  TTGTAACCGG  TCGTGTAGAG      400
CGCGGTATCG  TTAAAGTTGG  CGAAGAAGTT  GAAATCGTTG  GTATCAAAGA      450
GACTGCTAAG  TCTACCTGTA  CTGGCGTTGA  AATGTTCCGC  AAACTGCTGG      500
ACGAAGGCCG  TGCTGGTGAG  AACGTTGGTG  TTCTGCTGCG  TGGTATCAAA      550
CGTGAAGAAA  TCGAACGTGG  TCAGGTACTG  GCTAAGCCAG  GCTCAATCAA      600
GCCGCACACC  AAATTCGAAT  CTGAAGTTTA  TATTCTGTCC  AAAGATGAAG      650
GCGGCCGTCA  TACTCCGTTC  TTCAAAGGCT  ACCGTCCACA  GTTCTACTTC      700
CGTACAACTG  ACGTGACCGG  CACCATCGAA  CTGCCAGAAG  GCGTAGAGAT      750
GGTAATGCCA  GGCGACAACA  TTCAGATGGT  TGTTACCCTG  ATCCACCCAA      800
TCGCGATGGA  TGACGGTCTG  CGTTT                                  825
```

2) INFORMATION FOR SEQ ID NO: 52

     (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 822 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Enterobacter asburiae*
       (B)   STRAIN: ATCC 35953

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC          50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTT CATCATCGTG         100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT         150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG         200
ATACTCCAAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA         250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT         300
CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG         350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG         400
CGCGGTATCA TCAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA         450
GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG         500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA         550
CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA         600
GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG         650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC         700
CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT         750
GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA         800
TCGCGATGGA CGACGGTCTG CG                                       822
```

2) INFORMATION FOR SEQ ID NO: 53

     (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 826 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Enterobacter cancerogenus*
       (B)   STRAIN: ATCC 35317

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC          50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG         100
TTCCTGAACA AGTGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT         150
AGAAATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCAGGCGACG         200
ACACTCCAAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAAGCT         250
```

33

```
     GAGTGGGAAG  CAAAAATCAT  CGAACTGGCT  GGCTTCCTGG  ATTCTTACAT        300
     CCCAGAACCA  GAGCGTGCGA  TTGACAAGCC  ATTCCTGCTG  CCAATCGAAG        350
     ACGTATTCTC  CATCTCCGGT  CGTGGTACCG  TTGTTACCGG  TCGTGTAGAG        400
     CGCGGTATCA  TCAAAGTTGG  TGAAGAAGTT  GAAATCGTTG  GTATCAAAGA        450
  5  TACTGCKAAA  TCTACCTGTA  CTGGCGTTGA  AATGTTCCGC  AAACTGCTGG        500
     ACGAAGGCCG  TGCTGGTGAG  AACGTTGGTG  TTCTGCTGCG  TGGTATCAAA        550
     CGCGAAGAAA  TCGAACGTGG  TCAGGTTCTG  GCGAAGCCAG  GCTCAATCAA        600
     GCCACACACC  AAGTTCGAAT  CTGAAGTGTA  CATCCTGTCC  AAAGACGAAG        650
     GCGGCCGTCA  TACTCCGTTC  TTCAAAGGCT  ACCGTCCACA  GTTCTACTTC        700
 10  CGTACAACTG  ACGTGACCGG  TACCATCGAA  CTGCCAGAAG  GCGTAGAGAT        750
     GGTAATGCCA  GGCGACAACA  TCAAGATGGT  TGTGACGCTG  ATCCACCCAA        800
     TCGCGATGGA  CGACGGTCTG  CGTTTC                                   826
```

15

2) INFORMATION FOR SEQ ID NO: 54

          (i) SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 806 bases
 20   (B)   TYPE: Nucleic acid
              (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear

         (ii) MOLECULE TYPE: Genomic DNA
 25
         (vi) ORIGINAL SOURCE:
              (A)   ORGANISM: *Enterobacter cloacae*
              (B)   STRAIN: ATCC 13047

 30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

```
     GATCCTGGTA  GTAGCTGCGA  CTGACGGCCC  AATGCCTCAG  ACTCGTGAGC         50
     ACATCCTGCT  GGGTCGTCAG  GTAGGCGTTC  CTTACATCAT  CGTGTTCCTG        100
     AACAAATGCG  ACATGGTTGA  TGACGAAGAG  CTGCTGGAAC  TGGTAGAGAT        150
 35  GGAAGTTCGT  GAACTGCTGT  CTCAGTACGA  TTTCCCAGGC  GACGATACCC        200
     CAATCGTTCG  TGGTTCTGCT  CTGAAAGCGC  TGGAAGGCGA  CGCAGAGTGG        250
     GAAGMGAAAA  TCATCGAACT  GGCTGGCTAC  CTGGATTCTT  ACATCCCAGA        300
     ACCAGAGCGT  GCGATTGAYA  AGCCATTCCT  GCTGCCAATC  GAAGACGTAT        350
     TCTCCATCTC  CGGTCGTGGT  ACCGTTGTTA  CCGGTCGTGT  AGAGCGCGGT        400
 40  ATCATCAAAG  TGGGTGAAGA  AGTTGAAATC  GTTGGTATCA  AAGAGACTGC        450
     GAAGTCTACC  TGTACTGGCG  TTGAAATGTT  CCGCAAACTG  CTGGACGAAG        500
     GCCGTGCTGG  TGAGAACGTT  GGTGTTCTGC  TGCGTGGTAT  CAAACGTGAA        550
     GAAATCGAAC  GTGGTCAGGT  TCTGGCGAAG  CCAGGCTCAA  TCAAGCCACA        600
     CACCAAGTTC  GAATCTGAAG  TGTACATCCT  GTCCAAAGAC  GAAGGCGGCC        650
 45  GTCATACTCC  GTTCTTCAAA  GGCTACCGTC  CACAGTTCTA  CTTCCGTACA        700
     ACTGACGTGA  CCGGTACCAT  CGAACTGCCA  GAAGGCGTAG  AGGTGGTAAT        750
     GCCAGGCGAC  AACATCAAGA  TGGTTGTGAC  TCTGATCCAC  CCAATCGCGA        800
     TGGACG                                                          806
```

50

2) INFORMATION FOR SEQ ID NO: 55

          (i) SEQUENCE CHARACTERISTICS:
 55   (A)   LENGTH: 826 bases
              (B)   TYPE: Nucleic acid
              (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear

 60   (ii) MOLECULE TYPE: Genomic DNA

                                       34

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Enterobacter gergoviae*
    (B)   STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

```
CGGCGCGATC  CTGGTTGTTG  CTGCGACTGA  CGGCCCGATG  CCGCAGACCC        50
GTGAGCACAT  CCTGCTGGGT  CGTCAGGTAG  GCGTTCCGTA  CATCATCGTG       100
TTCCTGAACA  AGTGCGACAT  GGTTGATGAC  GAAGAGCTGC  TGGAACTGGT       150
AGAGATGGAA  GTTCGTGAAC  TGCTGTCTCA  GTACGATTTC  CCGGGCGACG       200
ACACCCCGAT  CGTTCGCGGT  TCTGCGCTGA  AAGCGCTGGA  AGGCGACGCA       250
GAGTGGGAAG  CGAAAATCAT  CGAACTGGCT  GGCCACCTGG  ATACCTAYAT       300
CCCGGAACCA  GAGCGTGCGA  TTGACAAGCC  GTTCCTGCTG  CCGATCGAAG       350
ACGTATTCTC  CATTTCCGGT  CGTGGTACCG  TTGTTACCGG  TCGTGTAGAG       400
CGCGGTATCA  TCAAGGTTGG  TGAAGAAGTT  GAAATCGTTG  GTATCAAAGA       450
CACCGCGAAA  ACCACCTGTA  CTGGCGTTGA  AATGTTCCGC  AAACTGCTGG       500
ACGAAGGCCG  TGCTGGTGAG  AACGTCGGCG  TTCTGCTGCG  TGGTATCAAG       550
CGTGAAGAAA  TCGAACGTGG  TCAGGTACTG  GCTAAGCCGG  GCTCCATCAA       600
GCCGCACACC  AAGTTCGAAT  CTGAAGTGTA  CATCCTGTCC  AAAGACGAAG       650
GCGGCCGTCA  CACTCCGTTC  TTCAAAGGCT  ACCGTCCGCA  GTTCTACTTC       700
CGTACAACTG  ACGTGACTGG  CACCATCGAA  CTGCCGGAAG  GCGTAGAGAT       750
GGTAATGCCG  GGCGACAACA  TCAAGATGGT  TGTTACCCTG  ATCCACCCGA       800
TCGCGATGGA  CGACGGTCTG  CGTTTC                                   826
```

2) INFORMATION FOR SEQ ID NO: 56

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 829 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Enterobacter hormaechei*
        (B)   STRAIN: ATCC 49162

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

```
GGCGCGATCC  TGGTTGTTGC  TGCGACTGAC  GGCCCTATGC  CTCAGACCCG        50
TGAGCACATC  CTGCTGGGTC  GTCAGGTAGG  CGTTCCTTAC  ATCATCGTGT       100
TCCTGAACAA  ATGCGACATG  GTTGATGACG  AAGAGCTGCT  GGAACTGGTA       150
GAGATGGAAG  TTCGTGAACT  GCTGTCTCAG  TACGATTTCC  CAGGCGACGA       200
CACCCCAATC  GTTCGTGGTT  CCGCGCTGAA  AGCGCTGGAA  GGCGAMGCAG       250
AGTGGGAAGM  GAAAATCATC  GARCTGGCTG  GCTTCCTGGA  TTCTTACATC       300
CCAGAACCAG  AGCGTGCGAT  TGACAAGCCA  TTCCTGCTGC  CAATCGAAGA       350
CGTATTCTCC  ATCTCCGGTC  GTGGTACCGT  TGTTACCGGT  CGTGTWGAGC       400
GCGGTATCAT  CAAAGTAGGT  GAAGAAGTTG  AAATCGTTGG  TATCAAAGAG       450
ACTGCGAAGT  CTACCTGTAC  TGGCGTTGAA  ATGTTCCGCA  AACTGCTGGA       500
CGAAGGCCGT  GCTGGTGAGA  ACGTTGGTGT  TCTGCTGCGT  GGTATCAAAC       550
GTGAAGAAAT  CGAACGTGGT  CAGGTTCTGG  CGAAGCCAGG  CTCAATCAAG       600
CCACACACCA  AGTTCGAATC  TGAAGTGTAC  ATTCTGTCCA  AAGACGAAGG       650
CGGCCGTCAT  ACTCCGTTCT  TCAAAGGCTA  CCGTCCACAG  TTCTACTTCC       700
GTACAACTGA  CGTGACCGGT  ACCATCGAAC  TGCCAGAAGG  CGTAGAGATG       750
GTAATGCCAG  GCGACAACAT  CAAGATGGTT  GTGACGCTGA  TCCACCCAAT       800
CGCGATGGAC  GACGGTCTGC  GTTTCGCAA                                829
```

2) INFORMATION FOR SEQ ID NO: 57

    (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 831 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
      (A)   ORGANISM: *Enterobacter sakazakii*
      (B)   STRAIN: ATCC 29544

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

```
GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT     150
GAGATGGAAG TGCGCGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA     200
CACCCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCTG     250
AGTGGGAAGC GAAAATCATC GAGCTGGCAG GTCACCTGGA TTCCTACATC     300
CCGGAACCGG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA     350
CGTATTCTCC ATCTCYGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAGGTTGGT GAAGAAGTTG AAATCGTGGG CATCAAAGAC     450
ACCGCGAAAT CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCGGGCGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCCATCAAG     600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG     650
CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     700
GTACRACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG     750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT     800
CGCGATGGAC GACGGTCTGC GTTTCGCAAT C                         831
```

2) INFORMATION FOR SEQ ID NO: 58

    (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 835 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
      (A)   ORGANISM: *Enterococcus casseliflavus*
      (B)   STRAIN: ATCC 25788

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

```
CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACAC      50
GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT     100
TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT     150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATATGACTTC CCAGGCGACG     200
ATGTTCCTGT AATCGCTGGT TCTGCTTTGA AAGCTCYTGA AGGCGATGCT     250
```

36

```
          TCATACGAAG AAAAAATCAT GGAATTAATG GCTGCAGTTG ACGAATACGT     300
          TCCAACTCCA GAACGTGACA CTGACAAACC ATTCATGATG CCAGTCGAAG     350
          ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
          CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTTG GTATTGCTGA     450
     5    AGAAACTGCT AAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTGT     500
          TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGTGTT     550
          GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT     600
          CACACCTCAT ACAAAATTTA AAGCTGAAGT TTACGTTTTA ACAAAAGAAG     650
          AAGGTGGACG TCACACACCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC     700
     10   TTCCGTACAA CTGACGTAAC TGGTGTTGTT GAATTACCAG AAGGAACTGA     750
          AATGGTTATG CCTGGTGATA ACGTAACAAT CGACGTTGAA TTGATCCACC     800
          CAATCGCTAT CGAAGACGGA ACTCGTTTCT CAATT                    835
```

     15
          2) INFORMATION FOR SEQ ID NO: 59

               (i) SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 826 bases
     20   (B)   TYPE: Nucleic acid
                    (C)   STRANDEDNESS: Double
                    (D)   TOPOLOGY: Linear

               (ii) MOLECULE TYPE: Genomic DNA
     25
               (vi) ORIGINAL SOURCE:
                    (A)   ORGANISM: *Enterococcus cecorum*
                    (B)   STRAIN: ATCC 43198

     30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

```
          GGTGCTATCT TAGTAGTATC TGCTGCTGAT GGTCCTATGC CACAAACTCG      50
          TGAACACATT CTTTTATCAC GTAACGTTGG TGTTCCATAC ATCGTTGTTT     100
          TCTTAAACAA AGTTGATATG GTTGACGACG AAGAATTATT AGAATTAGTT     150
     35   GAAATGGAAG TACGTGACTT ATTAACTGAA TACGACTTCC CAGGAGACGA     200
          TGTTCCTGTA ATCGCTGGTT CTGCATTAAA AGCTTTAGAA GGCGACCCAT     250
          CTTACGAAGA AAAAATCTTA GAATTAATGG CTGCAGTTGA CGAATACATC     300
          CCAACTCCAG AACGTGACAA CGATAAACCA TTCATGATGC CAGTCGAAGA     350
          CGTATTTTCA ATCACTGGTC GTGGTACTGT TGCTACAGGT CGTGTTGAAC     400
     40   GTGGACAAGT ACGTGTTGGT GACGAAGTTG AAATAGTTGG TATCCATGAT     450
          GAAATTTCTA AAACAACAGT TACTGGTGTT GAAATGTTCC GTAAATTATT     500
     AGATTACGCT GAAGCTGGAG ACAACATCGT TGCATTATTA CGTGGTGTGG      550
     CTCGTGAAGA TATCCAACGT GGTCAAGTAT TAGCTAAACC AGGTTCAATC     600
     ACTCCACATA CAAAATTCAC TGCTGAAGTG TACGTTTTAA CTAAAGAAGA     650
     45   AGGTGGACGT CATACTCCAT TCTTCACTAA CTACCGTCCA CAATTCTACT     700
     TCCGTACAAC TGACGTTACA GGTGTAGTTA ACTTACCAGA AGGTACTGAA     750
     ATGGTTATGC CTGGTGATAA CGTAACTATG GAAGTTGAAT TAATCCACCC     800
     AATCGCTATC GAAGACGGAA CTCGTT                               826
```

     50

          2) INFORMATION FOR SEQ ID NO: 60

               (i) SEQUENCE CHARACTERISTICS:
     55   (A)   LENGTH: 835 bases
                    (B)   TYPE: Nucleic acid
                    (C)   STRANDEDNESS: Double
                    (D)   TOPOLOGY: Linear

     60   (ii) MOLECULE TYPE: Genomic DNA
                                   37

```
        (vi) ORIGINAL SOURCE:
             (A)    ORGANISM: Enterococcus dispar
             (B)    STRAIN: ATCC 51266

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

        CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACTC    50
        GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTTCCTTA CATCGTCGTT   100
        TTCTTGAACA AAATGGACAT GGTTGATGAC GAAGAATTAT TAGAATTAGT   150
        TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG   200
        ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT   250
        TCATATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT   300
        CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG   350
        ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA   400
        CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA   450
        AGAAACTGCT AAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTGT   500
        TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG   550
        GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAAC CAGGTTCAAT   600
        CACTCCACAT ACAAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG   650
        AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC   700
        TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA   750
        AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC   800
        CAATCGCGAT CGAAGACGGT ACTCGTTTCT CAATC                   835


     2) INFORMATION FOR SEQ ID NO: 61

        (i) SEQUENCE CHARACTERISTICS:
             (A)    LENGTH: 835 bases
             (B)    TYPE: Nucleic acid
             (C)    STRANDEDNESS: Double
             (D)    TOPOLOGY: Linear

       (ii) MOLECULE TYPE: Genomic DNA

       (vi) ORIGINAL SOURCE:
             (A)    ORGANISM: Enterococcus durans
             (B)    STRAIN: ATCC 19432

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

        CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCCTATG CCTCAAACTC    50
        GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTTCCTTA CATCGTYGTA   100
        TTCTTGAACA AAGTAGATAT GGTCGATGAC GAAGAATTAC TAGAATTAGT   150
        TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG   200
        ATGTTCCTGT AATCGCTGGT TCAGCTTTGA AAGCTTTAGA AGGCGACGCT   250
        TCATACGAAG AAAAAATCCT TGAATTAATG GCTGCAGTTG ACGAATATAT   300
        CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG   350
        ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA   400
        CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA   450
        AGAAACAGCT CAAACAACAG TTACTGGTGT TGAAATGTTC CGTAAATTAT   500
        TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGTT   550
        GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT   600
        CACKCCTCAT ACAAAATTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG   650
        AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC   700
        TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA   750
        AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC   800
        CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC                   835
```

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2) INFORMATION FOR SEQ ID NO: 62

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 680 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Enterococcus faecalis*
       (B)   STRAIN: R610

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

```
AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT    50
TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA   100
ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT   150
TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA   200
TCGCAGGTTC TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA   250
AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA   300
ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA   350
TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT   400
CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA   450
AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG   500
AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT   550
ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC   600
AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC   650
ACACTCCATT CTTCACTAAC TACCGTCCTC                         680
```

2) INFORMATION FOR SEQ ID NO: 63

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 680 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Enterococcus faecalis*
       (B)   STRAIN: R487

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

```
AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT    50
TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA   100
ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT   150
TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA   200
TCGCAGGTTC TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA   250
AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA   300
ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA   350
TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT   400
```

39

```
      CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA          450
      AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG          500
      AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT          550
      ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC          600
  5   AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC          650
      ACACTCCATT CTTCACTAAC TACCGTCCTC                               680
```

10   2) INFORMATION FOR SEQ ID NO: 64

         (i) SEQUENCE CHARACTERISTICS:
             (A)   LENGTH: 685 bases
             (B)   TYPE: Nucleic acid
15   (C)   STRANDEDNESS: Double
             (D)   TOPOLOGY: Linear

         (ii) MOLECULE TYPE: Genomic DNA

20   (vi) ORIGINAL SOURCE:
             (A)   ORGANISM: *Enterococcus faecium*
             (B)   STRAIN: R482

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64
25
```
      AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACTCGT GAACACATCC           50
      TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA          100
      GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT          150
      TCGTGACCTA TTAACAGAAT ACGAATTCCC TGGTGACGAT GTTCCTGTAG          200
  30  TTGCTGGATC AGCTTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA          250
      AAAATTCTTG AATTAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA          300
      ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA          350
      TTACTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT          400
      CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AAACTTCAAA          450
  35  AACAACAGTT ACTGGTGTTG AAATGTTCCG TAAATTGTTA GACTACGCTG          500
      AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTTGC ACGTGAAGAC          550
      ATCCAACGTG GACAAGTTTT AGCTAAACCA GGTACAATCA CACCTCATAC          600
      AAAATTCTCT GCAGAAGTAT ACGTGTTGAC AAAAGAAGAA GGTGGACGTC          650
      ATACTCCATT CTTCACTAAC TACCGTCCTC AATTT                         685
  40
```

     2) INFORMATION FOR SEQ ID NO: 65

45   (i) SEQUENCE CHARACTERISTICS:
             (A)   LENGTH: 825 bases
             (B)   TYPE: Nucleic acid
             (C)   STRANDEDNESS: Double
             (D)   TOPOLOGY: Linear
50
         (ii) MOLECULE TYPE: Genomic DNA

         (vi) ORIGINAL SOURCE:
             (A)   ORGANISM: *Enterococcus flavescens*
55   (B)   STRAIN: ATCC 49996

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

```
      CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC           50
  60  GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT          100
```

```
     TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT         150
     TGAAATGGAA GTTCGTGACT TATTGTCAGA ATATGACTTC CCAGGCGACG         200
     ATGTTCCTGT AATCGCTGGT TCTGCTTTGA AAGCTCTTGA AGGCGATGCT         250
     TCATACGAAG AAAAAATCAT GGAATTAATG GCTGCAGTTG ACGAATACGT         300
  5  TCCAACTCCA GAACGTGACA CTGACAAACC ATTCATGATG CCAGTCGAAG         350
     ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA         400
     CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTTG GTATTGCTGA         450
     AGAAACTGCT AAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTGT         500
     TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGGGTT         550
 10  GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAG CTGGTACAAT         600
     CACACCTCAT ACAAAATTTA AAGCTGAAGT TTACGTTTTA ACAAAAGAAG         650
     AAGGTGGACG TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC         700
     TTCCGTACAA CTGACGTAAC TGGTGTTGTT GAATTACCAG AAGGAACTGA         750
     AATGGTTATG CCTGGTGATA AMGTAACAAT CGACGTTGAA TTGATCCACC         800
 15  CAATCGCTAT CGAAGACGGA ACTCG                                    825
```

2) INFORMATION FOR SEQ ID NO: 66

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 636 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Enterococcus gallinarum*
        (B)   STRAIN: R420

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

```
     TCCTATGCCT CAAACTCGTG AACACATCTT GTTATCACGT AACGTTGGCG          50
     TACCATACAT CGTTGTTTTC TTGAACAAAA TGGATATGGT TGATGACGAA         100
     GAATTGCTAG AATTAGTTGA AATGGAAGTT CGTGACCTAT TGTCTGAGTA         150
     TGACTTCCCA GGCGACGATG TTCCTGTAAT CGCCGGTTCT GCTTTGAAAG         200
     CTCTTGAAGG AGATCCTTCA TACGAAGAAA AAATCATGGA ATTGATGGCT         250
 40  GCAGTTGACG AATACGTTCC AACTCCAGAA CGTGATACTG ACAAACCATT         300
     CATGATGCCA GTCGAAGACG TATTCTCAAT CACTGGACGT GGTACTGTTG         350
     CTACAGGCCG TGTTGAACGT GGACAAGTTC GCGTTGGTGA TGAAGTAGAA         400
     ATCGTTGGTA TTGCTGACGA AACTGCTAAA ACAACTGTAA CAGGTGTTGA         450
     AATGTTCCGT AAAATTGTTAG ACTATGCTGA AGCAGGGGAT AACATTGGTG        500
 45  CATTGCTACG TGGGGTTGCT CGTGAAGACA TCCAACGTGG ACAAGTATTG         550
     GCTAAAGCTG GTACAATCAC ACCTCATACA AAATTCAAAG CTGAAGTTTA         600
     TGTTTTGACA AAAGAAGAAG GTGGACGTCA CACTCC                        636
```

2) INFORMATION FOR SEQ ID NO: 67

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 835 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

41

(vi)ORIGINAL SOURCE:
   (A)   ORGANISM: *Enterococcus hirae*
   (B)   STRAIN: ATCC 8043

5   (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 67

```
CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACTC        50
GTGAACATAT CCTAYTATCT CGTCAAGTTG GTGTTCCATA CATCGTTGTA       100
TTCTTGAACA AAGTAGATAT GGTTGACGAC GAAGAATTAC TAGAATTAGT       150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG       200
ATGTTCCTGT AGTTGCTGGT YCAGCTTTGA AAGCTTTAGA AGGCGACGCT       250
TCATACGAAG AAAAAATCCT TGAATTGATG GCTGCAGTTG ACGAATATAT       300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTCGAAG       350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA       400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA       450
AGAAACAGCT CAAACAACAG TTACTGGTGT TGAAATGTTC CGTAAATTAT       500
TAGACTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGTT       550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT       600
CACACCTCAT ACAAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAAGAAG       650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC       700
TTCCGTACRA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA       750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC       800
CAATCGCTAT CGAAAACGGT ACTAAATTCT CAATC                       835
```

2)INFORMATION FOR SEQ ID NO: 68

   (i)SEQUENCE CHARACTERISTICS:
     (A)   LENGTH: 835 bases
     (B)   TYPE: Nucleic acid
     (C)   STRANDEDNESS: Double
     (D)   TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:
   (A)   ORGANISM: *Enterococcus mundtii*
   (B)   STRAIN: ATCC 43186

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 68

```
CGGAGCAATC TTAGTTGTTT CTGCTGCTGA CGGCCCTATG CCTCAAACTC        50
GTGAACACAT CCTATTATCT CGTCAAGTTG GTGTACCATA CATCGTTGTA       100
TTCTTGAACA AAGTAGATAT GGTTGATGAC GAAGAATTAC TTGAATTAGT       150
TGAAATGGAA GTTCGTGACC TATTAACAGA ATACGAATTC CCTGGTGACG       200
ATGTTCCTGT AATCGCTGGT TCAGCTTTAA GAGCTTTAGA AGGCGACGCT       250
KCATACGAAG AAAAAATTCT TGAATTGATG GCTGCAGTTG ACGAATATAT       300
CCCAACTCCA GAACGTGATA ACGACAAACC ATTCATGATG CCAGTTGAGG       350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG ACGTGTTGAA       400
CGTGGACAAG YTCGTGTTGG TGACGTTATC GATATCGTTG GTATCGCAGA       450
AGAAACAGCT CAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTAT       500
TAGACTACGC TGAAGCAGGC GATAACATTG GTGCGTTACT ACGTGGTGTT       550
TCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTAAAC CAGGTACAAT       600
CACACCTCAT ACAAAATTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG       650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC       700
TTCYGTACGA CTGACGTAAC TRGTGTTGTY GAATTACCAG AAGGAACTGA       750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC       800
CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC                       835
```

2) INFORMATION FOR SEQ ID NO: 69

5   (i) SEQUENCE CHARACTERISTICS:
         (A)   LENGTH: 836 bases
         (B)   TYPE: Nucleic acid
         (C)   STRANDEDNESS: Double
         (D)   TOPOLOGY: Linear
10
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
         (A)   ORGANISM: *Enterococcus pseudoavium*
15   (B)   STRAIN: ATCC 49372

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

```
      CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACAC    50
20    GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCTTA CATCGYTGTA    100
      TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT    150
      TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGATTTC CCAGGCGACG    200
      ACACTCYAGT TATCGCTGGT TCAGCYTTGA AAGCTTTAGA AGGCGACCCT    250
      TCATACRAAG AAAAAATCTT AGAATTAATG SCTGCTGTTG ACGAATACAT    300
25    CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG    350
      ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA    400
      CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA    450
      AGAAACTGCT AAAACAACTG TTACAGGTGT TGAAATGTTC CGTAAATTGT    500
      TAGACTACGC TGAAGCAGGC GATAACATCG GTGCATTATT ACGTGGTGTT    550
30    GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT    600
      CACTCCACAT ACAAAATTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG    650
      AAGGCGGGCG TCACACTCCG TTCTTCACTA ACTACCGTCC TCAGTTCTAC    700
      TTCCGTACAA CTGACGTAAC TGGTGTTGTT GATCTACCAG AAGGTACTGA    750
      AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC    800
35    CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATTC                   836
```

2) INFORMATION FOR SEQ ID NO: 70
40
         (i) SEQUENCE CHARACTERISTICS:
         (A)   LENGTH: 835 bases
         (B)   TYPE: Nucleic acid
         (C)   STRANDEDNESS: Double
45   (D)   TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
50   (A)   ORGANISM: *Enterococcus raffinosus*
         (B)   STRAIN: ATCC 49427

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

```
55    CGGAGCTRTC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACTC    50
      GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCTTA CATCGTTGTA    100
      TTCTTAAACA AAATGGATAT GGTTGACGAT GAAGAATTAC TAGAATTAGT    150
      TGAAATGGAA GTTCGTGACT TATTAACTGA ATACGACTTC CCAGGCGACG    200
      ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT    250
60    TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ATGAATACAT    300
```

43

```
        CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGYGGAAG    350
        ACGTAYTCTC AATCACTGGT CGTGGAACTG TTGCAACTGG TCGTGTTGAA    400
        CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATTGCTGA    450
        AGAAACTGCT AAAACAACTG TTACAGGTGT TGAAATGTTC CGTAAATTGT    500
   5    TGGATTACGC TGAAGCGGGC GACAACATTG GTGCATTATT ACGTGGTGTT    550
        GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT    600
        CACTCCACAT ACAAAATTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG    650
        AAGGCGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC    700
        TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA    750
  10    AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC    800
        CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATT                   835
```

15 2) INFORMATION FOR SEQ ID NO: 71

        (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 835 bases
            (B)   TYPE: Nucleic acid
20   (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

       (ii) MOLECULE TYPE: Genomic DNA

25   (vi) ORIGINAL SOURCE:
            (A)   ORGANISM: *Enterococcus saccharolyticus*
            (B)   STRAIN: ATCC 43076

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71
30

```
        CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACTC    50
        GTGAACACAT CTTGTTATCT CGTAACGTAG GTGTTCCTTA CATCGTTGTA    100
        TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAT TAGAATTAGT    150
        AGAAATGGAA GTTCGTGACT TATTATCAGA ATACGATTTC CCAGGCGATG    200
  35    ACACTCCAGT TATTGCAGGT TCTGCTTTGA AAGCTTTAGA AGGCGATCCA    250
        GTTTACGAAG AAAAAATCTT CGAATTAATG GCTGCAGTTG ACGAATATAT    300
        CCCAACTCCA GAACGTGATA CTGAAAAACC ATTCATGATG CCAGTTGAGG    350
        ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA    400
        CGTGGACAAG TTCGCGTTGG TGACGTTGTA GAAATCGTTG GTATCGACGA    450
  40    AGAAACAGCT CAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTAT    500
        TAGACTACGC TGAAGCAGGC GATAACATCG GTGCTTTATT ACGTGGGGTT    550
        GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAC CAGGAACAAT    600
        CACTCCTCAT ACAAAATTCG TAGCTGAAGT TTACGTTTTA ACTAAAGAAG    650
        AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC    700
  45    TTCCGTACAA CTGACGTAAC TGGTGTTGTA GAATTACGCG AAGGTACTGA    750
        AATGGTAATG CCTGGTGACA ACGTAACTAT CGACGTTGAA TTAATCCACC    800
        CAATCGCTAT CGAAGACGGA ACTCGTTTCT CTATT                   835
```

50
   2) INFORMATION FOR SEQ ID NO: 72

        (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 823 bases
55   (B)   TYPE: Nucleic acid
            (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

       (ii) MOLECULE TYPE: Genomic DNA
60

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Enterococcus solitarius*
    (B)   STRAIN: ATCC 49428

5   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

```
GAGCTATCTT GGTAGTTTCT GCAGCTGATG GCCCAATGCC ACAAACTCGT      50
GAACATATTT TGTTGTCACG TAATGTAGGT GTACCTTACA TCGTTGTGTT     100
CTTGAACAAA ATGGATATGG TTGATGACGA AGAATTACTT GAGTTAGTTG     150
AAATGGAAGT ACGTGATCTA TTATCTGAAT ACGACTTCCC AGGAGATGAT     200
ACTCCAGTTA TTTCCGGTTC AGCTTTGAAA GCTTTAGAAG GCGACGAAGA     250
ATATGAACAA AAAATTATGG ACTTAATGGA TGCAGTTGAT GACTACATTC     300
CAACTCCTGA ACGTGACCAT GACAAACCAT TCATGATGCC AATTGAAGAT     350
GTATTTTCAA TTACAGGCCG TGGTACTGTT GCTACAGGAC GTGTTGAACG     400
CGGGACTATC AAAGTCGGCG ATGAAGTTGA CATTATTGGT ATTCATGAAG     450
ACGTTAAAAA GACAACAGTT ACTGGTGTAG AAATGTTCCG TAAATTGTTG     500
GACTACGCTG AAGCAGGCGA TAACATTGGT ACTTTGTTAC GTGGTGTTTC     550
TCGTGATGAT ATCGAACGTG GTCAAGTATT AGCTAAACCA GGTTCAATCA     600
CACCACATAC AAGATTCTCT GCTGAAGTTT ATGTTTTGAC TAAAGAAGAA     650
GGCGGACGTC ATACTCCATT CTTCTCAAAC TATCGTCCTC AATTCTACTT     700
CCGTACAACT GATATCACTG GTGTCATTGA ATTGCCAGAA GGTACTGAAA     750
TGGTAATGCC AGGTGATAAT GTAACAATGG ATGTTGAATT AATCCACCCA     800
GTCGCTATCG AAGAAGGAAC TCG                                  823
```

2) INFORMATION FOR SEQ ID NO: 73

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 835 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Enterococcus casseliflavus*
        (B)   STRAIN: ATCC 25788

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

```
CGGTGCAATC TTGGTCGTAT CAGCGACAGA TGGCCCAATG CCACAAACAC      50
GGGAGCATAT TTTGCTTTCT CGTCAAGTGG GTGTGAAACA TTTGATCGTC     100
TTTTTGAATA AGACGGACCT TGTCGATGAT GACGAGTTGA TCGATTTAGT     150
TGAAATGGAA GTCAGAGAAT TGCTGACTGA ATATGATTTT CCTGGCGACG     200
ACATTCCTGT GATCAAGGGC TCTGCGTTAA AAGCCTTGGA AGGGGACCCA     250
GATGCTGAAG CAGCGATCTT AACGCTGATG GATACAGTAG ATGAATATAT     300
CCCAACGCCA GAACGTGATA CTGACAAACC ATTGTTGTTA CCGATCGAAG     350
ATGTCTTTTC GATCACAGGA CGGGGGACCG TTGCTTCTGG TCGGATCGAT     400
CGCGGCATGG TAAAAGTCGG GGATGAAGTA GAAATCGTCG GAATCAAACC     450
TGAAACACAA AAAGCAGTCG TGACAGGGGT AGAAATGTTC CGCAAAACGA     500
TGGACTTCGG AGAAGCTGGC GATAACGTAG GGGTATTGTT ACGGGGCATC     550
ACCCGTGATG AAATTGAACG TGGCCAAGTG TTAGCAAAAC CAGGTTCTAT     600
CACACCGCAT ACGAAATTCC AAGCGGAAGT CTATGTGTTG ACAAAAGAAG     650
AAGGCGGTCG CCATACCCCA TTCTTTAATA ATTATCGCCC ACAATTTTAC     700
TTCCGTACAA CGGACGTAAC TGGGAATATC GTTTTACCAG AAGGAACGGA     750
AATGGTGATG CCTGGTGACA ACGTAACGAT CGATGTGGAA TTGATCCATC     800
CGATCGCTGT AGAAAATGGA ACGACCTTCT CGATT                     835
```

2) INFORMATION FOR SEQ ID NO: 74

     (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 380 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Staphylococcus saprophyticus*
       (B)   STRAIN: ATCC 15305

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

```
TAACGGGCGT CTCGATAGAA AAACACGTGA AAATCCCAAT GATTATAAAC    50
AATCAATATA CGATTTTGCT GAAGCTGTAA CAAAAGGTAT TAAGGAACAA   100
ACAAATAAAA ATTAATAGGC AACTTAACCA GAATCGTTAA AACTATATGA   150
AGATTCTGGT TTTTTAAATT CAAAAAGTTT TCTAAAAAAT TTACTTGCTT   200
TTTTAAGTAT AGGTATAAAA TACGATTGAT TAAAACAGTA AAGGAAATGA   250
ATCATGAAAC AATTAACTAA GCCTTTATAC TTTTACCTAT TACTTTTTAT   300
TACAACAACG CTGATTGGCG CGTTACTATT ATATTTGCCA ATCACAGGTA   350
AACATCCTAT TGATTTTGTG GACGCCCGTT                         380
```

2) INFORMATION FOR SEQ ID NO: 75

     (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 666 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Enterococcus flavescens*
       (B)   STRAIN: ATCC 49996

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

```
GCAATCTTGG TCGTATCAGC GACAGATGGC CCAATGCCAC AAACACGGGA    50
GCATATTTTG CTTTCTCGTC AAGTGGGTGT GAAACATTTG ATCGTCTTTT   100
TGAATAAGAC GGACCTTGTC GATGATGACG AGTTGATCGA TTTAGTTGAA   150
ATGGAAGTCA GAGAATTGCT GACTGAATAT GATTTTCCTG GCGACGACAT   200
TCCTGTGATC AAGGGCTCTG CGTTAAAAGC CTTGGAAGGG GACCCAGATG   250
CTGAAGCAGC GATCTTAACG CTGATGGATA CGGTAGATGA ATATATCCCA   300
ACGCCAGAAC GTGATACTGA CAAACCATTG TTGTTACCGA TCGAAGATGT   350
CTTTTCGATC ACAGGACGGG GGACCGTTGC TTCTGGTCGG ATCGATCGCG   400
GCATGGTAAA AGTCGGGGAT GAAGTAGAAA TCGTCGGAAT CAAACCTGAA   450
ACACAAAAAG CAGTCGTGAC AGGGGTAGAA ATGTTCCGCA AAACGATGGA   500
CTTCGGAGAA GCTGGCGATA ACGTAGGGGT ATTGTTACGG GGCATCACCC   550
GTGATGAAAT TGAACGTGGC CAAGTGTTAG CAAAACCAGG TTCTATCACA   600
CCGCATACGA AATTCCAAGC GGAAGTCTAT GTGTTGACAA AAGAAGAAGG   650
CGGTCGCCAT ACCCCA                                        666
```

SUBSTITUTE SHEET (RULE 26)

2) INFORMATION FOR SEQ ID NO: 76

5   (i) SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 751 bases
              (B)   TYPE: Nucleic acid
              (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear
10
        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
              (A)   ORGANISM: *Enterococcus gallinarum*
15   (B)   STRAIN: ATCC 49573

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

```
        TGGTGCGATT  TTAGTTGTAT  CCGCAACAGA  TGGTCCAATG  CCTCAAACCC      50
20      GGGAACATAT  CTTGCTTTCG  AGACAAGTTG  GTGTGAAACA  TCTGATTGTT     100
        TTCTTGAACA  AAATCGATTT  AGTCGATGAC  GAAGAATTGA  TTGATTTAGT     150
        AGAAATGGAA  GTAAGAGAAC  TGCTATCTGA  ATATAATTTT  CCAGGGGATG     200
        ACATTCCTGT  TATCAAAGGT  TCGGCATTAA  AAGCGTTGGA  AGGAGACCCT     250
        GATGCAGAAG  CTGCCATCAT  GGAATTAATG  GATACAGTAG  ACAGCTATAT     300
25      CCCAACACCT  GAGCGTGATA  CAGACAAACC  ATTACTCTTG  CCAGTTGAAG     350
        ATGTCTTTTC  GATTACTGGA  CGAGGAACAG  TTGCTTCCGG  ACGGATCGAT     400
        CGGGGAACAG  TTCGGGTAGG  CGATGAAGTA  GAAATCGTCG  GTATCAAACC     450
        TGAAACCCAA  AAAGCTGTAG  TGACAGGCGT  CGAAATGTTC  CGCAAGACGA     500
        TGGACTTTGG  GGAAGCCGGT  GACAATGTAG  GTGTCTTGCT  GAGAGGGATC     550
30      ACTCGTGACG  AAATTGAACG  AGGACAAGTG  TTGGCTAAAC  CAGGTTCGAT     600
        CACACCACAT  ACAAAATTCC  AAGCAGAAGT  TTATGTATTG  ACGAAAGAAG     650
        AAGGTGGTCG  TCATACACCA  TTCTTCAACA  ACTATCGTCC  ACAATTTTAT     700
        TTCCGTACAA  CGGATGTGAC  AGGGAACATT  ACATTGCCTG  AAGGAACAGA     750
        A                                                             751
35
```

2) INFORMATION FOR SEQ ID NO: 77

40   (i) SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 834 bases

              (B)   TYPE: Nucleic acid
              (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear
45
        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
              (A)   ORGANISM: *Ehrlichia canis*
50   (B)   STRAIN: Florida

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

```
        TGCAGCAATA  TTAGTAGTGT  CTGCAACTGA  TGGAGCAATG  CCACAAACAA      50
55      GAGAACATAT  ATTATTAGCA  AAGCAAGTAG  GTGTAAAAGA  TATAGTAGTG     100
        TGGATGAATA  AGTGTGATGT  TGTAGATGAT  GAAGAAATGT  TGTCATTAGT     150
        TGAAATGGAA  ATAAGGGAAT  TGTTATCAAA  ATATGGGTAT  CCTGGGGATG     200
        ATATAGATGT  AGTTAGAGGA  TCTGCAGTTA  AAGCATTAGA  AGAAGAAACA     250
        GGCTCAGGTG  TGTGGAGTGA  AAAAATAATG  GAATTGATGA  ATGCTTTAGA     300
60      AAAAATAAGT  TTACCAGTAA  GAGAAAAAGA  TAAGCCATTT  TTAATGTCAA     350
```

47

```
     TAGAAGATGT GTTTTCAATA CCTGGAAGAG GTACAGTAGT AACAGGAAGA      400
     ATAGAAAGAG GAGTAATTAG AGTAGGGGAT AAAATAGAGA TAGTAGGATT      450
     GCGTGAGATA CAAAGTACAG TATGTACAGG TGTTGAAATG TTTCATAAAG      500
     CATTAGATGC AGGAGAAGCA GGGGATAATG CTGGAATATT GTTAAGAGGG      550
  5  ATAAAAAAAG AAGATGTAGA AAGAGGGCAA GTATTGAGTG CACCTGGACA      600
     GATACATTCA TATAAGAGAT TTAAGGCAGA GGTATATATA TTGAAAAAAG      650
     AAGAAGGAGG AAGACATACT CCATTTTTCT CAAATTACCA GCCGCAATTT      700
     TATGTTAGAA CAACAGATGT AACAGGGAAT ATAAAGTTAC CAGAAGGAGT      750
     AGAAATGGTA ATGCCAGGGG ATAATATAAA TATCGAAGTG AGTTTGGATA      800
 10  AGCCTGTTGC TATTGATCAA GGATTGAGAT TTGC                      834
```

2) INFORMATION FOR SEQ ID NO: 78

15

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 817 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
20   (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
25   (A)   ORGANISM: *Escherichia coli*
        (B)   STRAIN: ATCC 23511

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

```
 30  CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC       50
     GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
     TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT      150
     TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
     ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
 35  GAGTGGGAAG CGAAAATCCT GGAACTGGCT GGCTTCCTGG ATTCTTAYAT      300
     TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
     ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
     CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
     GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG      500
 40  ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
     CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
     GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
     GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
     CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
 45  GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA      800
     TCGCGATGGA CGACGGT                                         817
```

50 2) INFORMATION FOR SEQ ID NO: 79

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 825 bases
        (B)   TYPE: Nucleic acid
55   (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

60   (vi) ORIGINAL SOURCE:

48

SUBSTITUTE SHEET (RULE 26)

(A)   ORGANISM: *Escherichia fergusonii*
(B)   STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

```
CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG      50
CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTCCT     100
GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA     150
TGGAAGTTCG TGAACTTCTG TCTCAGTACG ACTTCCCGGG CGACGACACT     200
CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG     250
GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG     300
AACCAGAGCG TGCGATTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG     350
TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG     400
TATCATCAAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC     450
AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAAACT GCTGGACGAA     500
GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA     550
AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC     600
ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCCAAAGA TGAAGGCGGT     650
CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC     700
TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA     750
TGCCGGGCGA CAACATCAAA ATGGTTGTTA CCCTGATCCA CCCGATCGCG     800
ATGGACGACG GTCTGCGTTT CGCAA                                825
```

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:
    (A)   LENGTH: 829 bases
    (B)   TYPE: Nucleic acid
    (C)   STRANDEDNESS: Double
    (D)   TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A)   ORGANISM: *Escherichia hermannii*
    (B)   STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

```
GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT     150
GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA     200
CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG     250
AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC     300
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA     350
CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT     450
ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG     600
CCKCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     700
GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG     750
GTAATGCCGG CGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT     800
CGCGATGGAC GACGGTCTGC GTTTCGCAA                            829
```

SUBSTITUTE SHEET (RULE 26)

2) INFORMATION FOR SEQ ID NO: 81

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 816 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Escherichia vulneris*
       (B)   STRAIN: ATCC 33821

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC    50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG   100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT   150
TGAGATGGAA GTGCGTGAAC TTCTGTCCCA GTACGACTTC CCGGGCGACG   200
ACACCCCGAT CATTCGTGGT TCTGCGCTGA AAGCGCTGGA AGGCGAAGCT   250
GAGTGGGAAG AGAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCCTACAT   300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG   350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG   400
CGCGGTATCA TCAARGTKGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA   450
TACTGCGAAA TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG   500
ACGAAGGTCG TGCAGGCGAG AACTGCGGCG TTCTGCTGCG TGGTATCAAG   550
CGTGAAGAGA TCCAGCGTGG CCAGGTTCTG GCTAAGCCGG GCTCAATCAA   600
GCCGCACACC AAGTTCGAAT CCGAAGTGTA CATCCTGTCC AAAGACGAAG   650
GCGGCCGTCA CACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC   700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT   750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCATCCGA   800
TCGCGATGGA CGACGG                                        816
```

2) INFORMATION FOR SEQ ID NO: 82

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 828 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Eubacterium lentum*
       (B)   STRAIN: ATCC 43055

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

```
CGGCGCCTCC TCGTTATCGC CGCCACCGAC GGCCCGATGG CCCAGACCCG    50
CGAGCACATC CTGCTCGCCC GTCAGGTCGG CGTGCCCTAC ATCGTGGTCT   100
TCCTGAACAA GTGCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC   150
GAGATGGAAG TTCGCGAGCT GCTCGACTCT TACGAGTTCC CGGGCGACGA   200
CACCCCGATC ATCCGCGGCT CCGCTTTGAA GGCCCTCGAG GGCGACAAAG   250
AGTGGCAGGA GAAGGTCTGG GAGCTCATGG ACGCCGTCGA CTCCTACATC   300
CCGACGCCGG AGCGCATGGT CGACAAGCCG TTCCTGATGG CCGTCGAGGA   350
```

```
          CACGATGACC ATCACCGGCC GCGGCACCGT TGCCACCGGT CGTGTGGAGC          400
          GTGGTACGCT GCATGTCAAC GACCCGCTGG AGATCGTCGG TATCAAGGAG          450
          ACCCAGAACA CGGTCTGCAC CGGTATCGAG ATGTTCCGCA AGCTGCTCGA          500
          CGAGGCTCAG GCCGGCGACA ACATCGGCTG CCTGCTCCGC GGTGTCAAGC          550
   5      GCGAGGAGAT CGTTCGCGGC CAGGTTCTCT GCAAGCCCGG TAGCGTGACC          600
          CCGCACACCG AGTTCGAGGG TCAGGTCTAC ATCCTGACGA AGGAAGAGGG          650
          CGGCCGCCAC ACGCCGTTCT TCGACGGCTA CCGTCCGCAG TTCTACTTCC          700
          GCACGACGGA CGTGACGGGT GTTGCCCACC TTCCCGAGGG CACCGAGATG          750
          GTCATGCCGG CGACAACGT GGAGATCAAG GGCGAGCTCA TTCACCCGAT           800
  10      CGCCAGGAAG AGGGCTGCGT TCGCTAAC                                828
```

2) INFORMATION FOR SEQ ID NO: 83

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 835 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Eubacterium nodatum*
        (B)   STRAIN: ATCC 33099

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

```
  30      GGAGCAATTC TGGTTTGTGC AGCAACKGAC GGACCAATGC CTCAGACAAG           50
          AGAACATATC CTTTTGTCAA GGCAGGTAGG AGTGCCATAT ATCATCGTAT          100
          TCCTGAATAA ATGTGACATG GTGGATGAYG AAGAGCTTCT GGACTTGGTA          150
          GAGATGGAAG TAAGAGAACT TCTCAGTGAG TATGAATTCC CGGGAGATGA          200
          TACCCCGATA GTAAGAGGTT CAGCCCTGAA GGCACTGGAA GAACCCAATG          250
  35      GAGAATGGGC AGACAAGATT GTAGAGCTGA TGGAGGAAGT AGATAAATAC          300
          ATTCCTGAAC CAAAGAGAGA TAACGACAAA CCGTTCCTGA TGCCTGTAGA          350
          GGACGTATTC TCAATAACAG GAAGAGGAAC AGTAGCGACA GGAAGRGTTG          400
          AAAGAGGAAT CCTGAAGGTC GGTGATGAAG TAGAAATCGT GGGAATGAGC          450
          GAAGAGAGAA GAAAGGTAGT AGTAACGGGA GTTGAAATGT TCAGAAAGCT          500
  40      TCTGGATGAA GCAGAGACAG GAGACAACAT CGGAGCACTG CTGAGAGGAG          550
          TTCAGAGAAC RGAGATCCAG AGAGGTCAGG TATTGGCRGC ACCTGGAACG          600
          ATCAACCCAC ATACAAAGTT CAAGGGTCAG GTATATGTAC TGAAGAAGGA          650
          AGAAGGAGGA AGGCATACGC CGTTCTTCAA YGGATACAGW CCACAGTTCT          700
          ACTTCAGAAC AACAGACGTA ACAGGAGATT TGCAGCTGCC GGAAGGARCA          750
  45      GAGATGTGCA TGCCGGGAGA TAATGTGGTA ATGAACRTCA GCCTGATCAC          800
          TCCGATTGCT ATAGAAGAGG GWCTGAGATT TGCCA                        835
```

50 2) INFORMATION FOR SEQ ID NO: 84

    (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 826 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

51

```
        (A)     ORGANISM: Ewingella americana
        (B)     STRAIN: ATCC 33852

     (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 84
  5
        GCGATCCTGG  TTGTTGCTGC  AACTGATGGC  CCTATGCCAC  AGACTCGTGA    50
        GCACATCCTG  TTGGGTCGYC  AGGTTGGCGT  TCCATTCATG  ATCGTATTCA   100
        TGAACAAATG  CGACATGGTT  GATGACGAAG  AGCTGCTGGA  ACTGGTAGAA   150
        ATGGAAGTTC  GYGAACTTCT  GTCTGCTTAC  GATTTCCCAG  GCGACGACAT   200
 10     CCCAGTTGTT  AAAGGTTCAG  CGCTGAAAGC  ACTGGAAGGC  GAAGCAGAGT   250
        GGGAAGCTAA  GATCATCGAG  CTGGCTGGCC  ACCTGGATAG  CTACATCCCA   300
        GAACCAGAGC  GTGCGATTGA  CAAGCCATTC  CTGCTGCCAA  TCGAAGACGT   350
        ATTCTCCATC  TCCGGTCGTG  GTACCGTTGT  TACCGGTCGT  GTAGAGCGCG   400
        GTATCATCAA  AGTTGGCGAA  GAAGTTGAAA  TCGTTGGTAT  CAAGGACACT   450
 15     GTTAAGTCTA  CTTGTACTGG  CGTTGAAATG  TTCCGCAAAC  TGCTGGACGA   500
        AGGCCGTGCY  GGTGAGAACG  TTGGTGTTCT  GCTGCGTGGT  ATCAAGCGTG   550
        AAGACATCGA  ACGTGGTCAG  GTTCTGGCTA  AACCAGGTTC  AATCAAACCA   600
        CACACCACWT  TYGACTCAGA  AGTTTATATC  CTGAGCAAAG  ATGAAGGCGG   650
        CCGTCATACT  CCGTTCTTCA  AAGGCTACCG  TCCACAGTTC  TACTTCCGTA   700
 20     CAACTGACGT  GACCGGTACC  ATCGAACTGC  CAGAAGGCGT  AGAGATGGTA   750
        ATGCCAGGTG  ACAACATCAA  CATGRTAGTT  ACCCTGATCC  ACCCAATCGC   800
        GATGGATGAC  GGTCTGCGTT  TCGCAA                                826
```

```
 25
     2)INFORMATION FOR SEQ ID NO: 85

        (i)SEQUENCE CHARACTERISTICS:
           (A)     LENGTH: 828 bases
 30        (B)     TYPE: Nucleic acid
           (C)     STRANDEDNESS: Double
           (D)     TOPOLOGY: Linear

     (ii)MOLECULE TYPE: Genomic DNA
 35
     (vi)ORIGINAL SOURCE:
           (A)     ORGANISM: Francisella tularensis
           (B)     STRAIN: LVS

 40  (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 85
```

```
        TGGTGCTATT  CTAGTATGTT  CTGCTGCGGA  TGGTCCTATG  CCACAAACTC    50
        GTGAGCACAT  TCTGCTTTCT  CGTCAAGTTG  GTGTACCAAA  AATCGTTGTT   100
        TTCTTAAACA  AGTGTGACAT  GGTTGATGAT  GAAGAGTTAT  TAGAGCTAGT   150
 45     TGAGATGGAA  GTTCGTGAGC  TTTTAGATCA  GTATGAGTTC  CCAGGTGATG   200
        ACACTCCAGT  TATTATGGGT  TCAGCTCTTA  GAGCTATTGA  AGGTGACGAA   250
        GCTTACGTTG  AGAAAATTGT  TGAGCTAGTT  CAAGCTATGG  ATGACTATAT   300
        TCCTGCTCCT  GAGCGTGATA  CTGAGAAGCC  ATTTATTCTT  CCGATCGAAG   350
        ATGTATTCTC  AATTTCAGGT  CGTGGTACTG  TTGTAACTGG  TCGTATTGAG   400
 50     CGCGGTGTAG  TTAACGTTGG  TGATGAAGTT  GAAGTTGTTG  GTATTCGTCC   450
        AACTCAAAAA  ACTACAGTAA  CTGGTGTGGA  AATGTTCCGT  AAGCTTTTAG   500
        ATAGAGGGGA  AGCTGGTGAT  AACGTTGGTA  TCCTAGTTCG  TGGACTTAAG   550
        AGAGATGATG  TTGAGCGTGG  ACAAGTATTA  TGTAAGCCAG  GTTCAATTAA   600
        GCCACATACT  AAGTTTGAAG  CTGAGGTTTA  TGTATTATCT  AAAGAAGAGG   650
 55     GTGGTAGACA  TACTCCATTC  TTCAAGGGAT  ATAGACCACA  ATTCTACTTC   700
        CGTACTACAG  ACATTACTGG  AGCTGTTGAG  CTTCCAGAGG  GTGTAGAAAT   750
        GGTTATGCCT  GGTGATAACG  TTAAGATGAC  TATCACTCTA  ATTAACCCAA   800
        TCGCTAGGAT  GAAGGGTTAC  GTTTTGCA                             828
```

 60

SUBSTITUTE SHEET (RULE 26)

2) INFORMATION FOR SEQ ID NO: 86

     (i) SEQUENCE CHARACTERISTICS:
5
        (A)   LENGTH: 829 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

10   (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
        (B)   STRAIN: ATCC 10953
15
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

```
CGGTGCTATC ATCGTAGKTG CTGCTACTGA TGGTCCGATG CCTCARACTC      50
GTGAGCAYAT CYTGCTGGCT CGTCAGGTAA ACGTWCCKAG ACTGGTTGTA     100
TTCATGAACA AGTGYGACAT GGTAGACGAC GCTGAAATGY TGGAACTCGT     150
TGAAATGGAA ATGCGTGAAC TGCTTTCAGC YTACGAATTC GAYGGYGACA     200
ACACTCCKTT CATTCAGGGT TCTGCTCTTG GTGCRTTGAA YGGCGTTGAA     250
AAGTGGGAAG AGAAGGTTAT GGANCTGATG GATGCTTGCG ACACTTGGAT     300
TCCTTTGCCT CCGCGTGATA TTGAYAAACC GTTCTTGATG CCGGTTGAAG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCTACTGG TCGTATCGAA     400
GCTGGTGTTA TCCATGTAGG TGACGAAGTT GAAATCCTCG GTTTGGGTGA     450
AGACAAGAAG TCTGTTGTAA CTGGTGTTGA AATGTTCCGC AAGTTGCTGG     500
ATCAAGGTGA AGCTGGTGAC AACGTAGGTY TGTTGCTCCG TGGTATCGAC     550
AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAGCCCG GTCAGATTAA     600
ACCTCACTCT AAGTTCAAAG CTTCTATCTA CGTTTTGAAG AAAGAAGAAG     650
GTGGTCGTCA CACTCCGTTC CACAACAAAT ACCGTCCTCA GTTCTATCTG     700
CGTACTATGG ACTGTACAGG TGAAATCWCT CTTCCGGAAG GAACTGAAAT     750
GGTAATGCCT GGTGATAACG TAGAAATCAC TGTAGAACTG ATCTACCCGG     800
TAGCATTGAA CGTAGGTTTG CGTTTCGCT                            829
```

35

2) INFORMATION FOR SEQ ID NO: 87

40   (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 828 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear
45
    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Gemella haemolysans*
50   (B)   STRAIN: ATCC 10379

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

```
CTATCTTAGT AATCGCTGCT ACAGATGGAC CAATGGCTCA AACTCGTGAG      50
CACATCCTAT TATCTCGTAA CGTTGGAGTA CCAAAAATCG TTGTATTCTT     100
AAACAAATGT GATATGGTTG ATGACGAAGA GTTATTAGAA TTAGTTGAAA     150
TGGAAGTTCG TGAACTATTA TCTGAATACG GATTCGACGG AGATGAACTA     200
CCAGTAATCA AAGGTTCTGC TCTTAAAGCT CTTGAAGGAG ATGCAGATGC     250
AGAAAAAGCT ATCATCGAAT TAATGGAAAC AGTTGACGAA TACATCCCAA     300
CTCCAGAACG TGATAACGCT AAACCATTCA TGATGCCAGT TGAGGACGTA     350
```

53

```
      TTCTCAATCA CAGGTCGTGG TACAGTTGCT ACTGGACGTG TTGAACGTGG       400
      ACAAGTTAAA GTTGGAGACG TAGTAGAAAT CGTTGGATTA ACTGAAGAAC       450
      CAGCTTCAAC .TACTGTAACA GGTGTTGAAA TGTTCCGTAA ATTATTAGAT       500
      TACGCTGAAG CAGGAGATAA CATCGGTGCA TTATTACGTG GTGTTGCTCG       550
 5    TGAAGACATC GAACGTGGAC AAGTTTTAGC AGCTCCTAAA ACAATCACTC       600
      CACACACTCA ATTCGTAGCT GACGTGTACG TATTATCTAA AGAAGAAGGT       650
      GGACGTCACA CTCCATTCTT CACAAACTAC CGTCCTCAAT TCTACTTCCG       700
      TACTACTGAC GTAACTGGTG TAGTTACTTT ACCAGAAGGT ACTGAAATGG       750
      TAATGCCTGG GGATAACGTA TCAATCAACG TAGAACTTAT TTCTCCAATC       800
 10   GCGATCGAAG AAGGAACTCG TTTCTCAA                               828
```

2)INFORMATION FOR SEQ ID NO: 88

 (i)SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 823 bases
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear

 (ii)MOLECULE TYPE: Genomic DNA

 (vi)ORIGINAL SOURCE:
  (A) ORGANISM: *Gemella morbillorum*
  (B) STRAIN: ATCC 27824

 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 88

```
      TCTTAGTAAT CGCTGCTACA GATGGTCCTA TGGCTCAAAC TCGTGAACAC        50
      ATCCTATTAT CTCGTAACGT TGGAGTACCT AAAATTGTTG TATTCTTAAA       100
      CAAATGTGAT ATGGTTGATG ACGAAGAGTT ATTAGAATTA GTAGAAATGG       150
      AAGTTCGTGA ACTATTATCT GAATACGGAT TTGATGGAGA TGAACTACCA       200
      GTAATCAAAG GTTCAGCTCT TAAAGCTCTT GAAGGAGATG CAGATGCTGA       250
 35   AAAAGCTATC ATCGAATTAA TGGAAACAGT TGACGAGTAC ATCCCAACTC       300
      CAGAACGTGA TAACGCTAAA CCATTTATGA TGCCAGTTGA GGACGTGTTC       350
      TCAATCACAG GTCGTGGTAC AGTTGCTACT GGACGTGTTG AACGTGGACA       400
      AGTTAAAGTT GGTGACGTAG TAGAAATCGT TGGATTAACT GAAGAACCAG       450
      CTTCAACTAC TGTAACAGGT GTTGAAATGT TCCGTAAATT ATTAGATTAC       500
 40   GCTGAAGCAG GAGATAACAT CGGTGCATTA TTACGTGGTG TTGCTCGTGA       550
      AGATATCGAA CGTGGACAAG TTTTAGCAGC TCCTAAAACA ATCACTCCAC       600
      ATACTCAATT CGTAGCTGAT GTGTACGTAT TATCTAAAGA AGAAGGTGGA       650
      CGTCACACTC CATTCTTCAC AAACTACCGT CCACAATTCT ACTTCCGTAC       700
      TACTGACGTA ACTGGTGTAG TTACTTTACC AGAAGGTACT GAAATGGTAA       750
 45   TGCCTGGGGA CAACGTATCA ATCAACGTAG AACTTATTTC TCCAATCGCT       800
      ATCGAAGAAG GAACTCGTTT CTC                                    823
```

2)INFORMATION FOR SEQ ID NO: 89

 (i)SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 829 bases
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear

 (ii)MOLECULE TYPE: Genomic DNA

 (vi)ORIGINAL SOURCE:

54

```
            (A)    ORGANISM: Haemophilus actinomycetemcomitans
            (B)    STRAIN: ATCC 33384

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

    GCTATCTTAG  TAGTAGCAGC  AACCGACGGT  CCTATGCCAC  AAACTCGTGA        50
    GCACATCTTA  TTAGGTCGCC  AAGTAGGTGT  TCCTTACATC  ATCGTATTCT       100
    TAAACAAATG  CGACATGGTA  GATGACGAAG  AGTTATTAGA  ATTAGTTGAA       150
    ATGGAAGTTC  GTGAACTTCT  TTCTCAATAT  GACTTCCCGG  GCGATGACAC       200
    CCCAATCGTA  CGCGGTTCTG  CATTAAAAGC  GCTTGAAGGC  GATGCCGCAT       250
    GGGAAGAAAA  AATCCTTGAA  TTAGCAAACC  ATTTAGATAC  TTACATCCCG       300
    GAACCTGAGC  GTGCTATCGA  CCAACCGTTC  CTTCTTCCAA  TTGAAGATGT       350
    GTTCTCTATC  TCCGGTCGTG  GTACCGTAGT  AACGGGTCGT  GTTGAGCGCG       400
    GTATCATCCG  TACCGGTGAT  GAAGTTGAAA  TCGTGGGTAT  CAAACCGACT       450
    GCAAAAACCA  CCGTAACCGG  TGTTGAAATG  TTCCGTAAAT  TACTTGACGA       500
    AGGTCGTGCG  GGTGAAAACA  TCGGTGCATT  ATTGCGTGGT  ACTAAACGTG       550
    AAGAAATCGA  ACGTGGTCAG  GTATTGGCGA  AACCGGGGTC  AATCACCCCG       600
    CACACTGACT  TCGAATCTGA  AGTGTACGTA  TTGTCCAAAG  AAGAAGGTGG       650
    TCGTCATACT  CCATTCTTCA  AAGGTTACCG  TCCACAATTC  TATTTCCGTA       700
    CAACTGACGT  AACCGGTACT  ATCGAGTTAC  CTGAAGGCGT  GGAAATGGTT       750
    ATGCCTGGCG  ATAACATCAA  AATGACCGTA  TCCTTAATTC  ACCCAATTGC       800
    GATGGACCAA  GGTTTACGTT  TCGCTATCG                               829
```

```
    2) INFORMATION FOR SEQ ID NO: 90

            (i) SEQUENCE CHARACTERISTICS:
                (A)    LENGTH: 833 bases
                (B)    TYPE: Nucleic acid
                (C)    STRANDEDNESS: Double
                (D)    TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
                (A)    ORGANISM: Haemophilus aphrophilus
                (B)    STRAIN: ATCC 33389

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

    TGGTGCTATC  TTAGTAGTAG  CAGCAACTGA  TGGTCCTATG  CCACAAACTC        50
    GTGAGCACAT  CTTATTAGGT  CGCCAAGTAG  GTGTTCCTTA  CATCATCGTA       100
    TTCTTAAACA  AATGCGACAT  GGTAGATGAC  GAAGAGTTAT  TAGAATTAGT       150
    TGAAATGGAA  GTTCGTGAAC  TTCTTTCTCA  ATATGACTTC  CCGGGTGATG       200
    ATACACCAAT  CGTACGTGGT  TCTGCATTAC  AAGCGTTAAA  CGGCGTTGCA       250
    GAATGGGAAG  AAAAAATCCT  TGAATTAGCA  AACCACTTAG  ATACTTACAT       300
    TCCTGAGCCA  CAACGTGCTA  TCGACCAACC  GTTCCTTCTT  CCAATTGAAG       350
    ACGTGTTCTC  TATCTCCGGT  CGTGGTACTG  TAGTAACAGG  TCGTGTTGAG       400
    CGTGGTATCA  TCCGTACCGG  TGATGAAGTT  GAAATCGTAG  GTATCAAACC       450
    GACTGCGAAA  ACTACCGTAA  CCGGTGTTGA  AATGTTCCGT  AAATTACTTG       500
    ACGAAGGTCG  TGCAGGTGAA  AACATCGGTG  CATTATTACG  TGGCACTAAA       550
    CGTGAAGAAA  TCGAACGTGG  TCAAGTATTG  GCTAAACCGG  GCTCAATCAC       600
    TCCGCACACT  GATTTCGAAT  CTGAAGTGTA  CGTATTATCC  AAAGAAGAAG       650
    GTGGTCGTCA  TACTCCATTC  TTCAAAGGTT  ACCGTCCACA  ATTCTATTTC       700
    CGTACAACTG  ACGTAACCGG  TACTATCGAG  TTACCGGAAG  GCGTGGAAAT       750
    GGTTATGCCT  GGCGATAACA  TCAAAATGAC  TGTATCCTTA  ATCCACCCAA       800
    TCGCGATGGA  CCAAGGTTTA  CGTTCGCTA  TCG                          833
```

2) INFORMATION FOR SEQ ID NO: 91

     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 815 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Haemophilus ducreyi*
        (B)   STRAIN: DSM 8925

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

```
CGGCGCTATC TTAGTTGTAG CAGCAACTGA TGGTCCTATG CCTCAAACTC      50
GTGAACACAT CTTATTAGGC CGCCAAGTTG GTGTTCCTTA CATCATCGTA     100
TTCTTAAATA AATGCGATAT GGTAGATGAT GAAGAATTAT TAGAATTAGT     150
TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGATTTC CCAGGTGACG     200
ATACTCCTAT CGTTCGTGGT TCAGCATTAC AAGCATTAAA TGGTGTGCCT     250
GAGTGGGAAG AAAAAATCAT TGAATTAGCA CAACACTTAG ATTCTTATAT     300
CCCTGAGCCT GAGCGTGCGA TTGATAAACC TTTCTTATTA CCAATCGAAG     350
ACGTATTCTC AATTTCAGGT CGTGGTACAG TAGTAACCGG TCGTGTTGAG     400
CGTGGTATCA TCAAATCAGG TGAAGAAGTT GAAATCGTAG GGATTAAAGA     450
AACGACAAAA ACAACAGTAA CCGGTGTTGA GATGTTCCGT AAACTATTAG     500
ACGAAGGTCG TGCGGGTGAA AACGTAGGTG CCTTATTACG TGGTACTAAA     550
CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTACAATTAC     600
ACCACACACT GATTTTGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ATCGTCCTCA GTTCTACTTC     700
CGYACAACGG ACGTAACAGG AACGATTGAA TTACCTGAAG ATGTTGAGAT     750
GGTAATGCCT GGTGATAATA TCAAGATGAC AGTAAGCTTA ATTCACCCTA     800
TCGCGATGGA CGAAG                                          815
```

2) INFORMATION FOR SEQ ID NO: 92

     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 830 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Haemophilus haemolyticus*
        (B)   STRAIN: ATCC 33390

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

```
TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCAATG CCACAAACTC      50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCATA CATCATCGTA     100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT     150
AGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCAGGTGACG     200
ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCATTAAA TGGCGTAGCA     250
GAATGGGAAG AAAAAATCCT TGAGTTAGCA AACCACTTAG ATACTTACAT     300
CCCAGAACCA GAGCGTGCAA TTGACCAACC GTTCCTTCTT CCAATCGAAG     350
```

56

```
      ATGTGTTCTC AATCTCAGGT CGTGGTACAG TAGTAACTGG TCGTGTAGAA    400
      CGTGGTATCA TCCGTACTGG TGATGAAGTA GAAATCGTAG GTATCAAAGA    450
      TACAGCAAAA ACTACTGTAA CGGGTGTTGA AATGTTCCGT AAATTACTTG    500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAAA    550
  5   CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTTCAATCAC    600
      GCCACACACT GACTTCGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG    650
      GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC    700
      CGTACAACTG ACGTAACTGG TACTATCGAG TTACCAGAAG GCGTAGAAAT    750
      GGTAATGCCA GGCGATAACA TCAAGATGAC AGTAAGCTTA ATCCACCCAA    800
  10  TCGCGATGGA CCAAGGTTTA CGTTTCGCAA                          830
```

2) INFORMATION FOR SEQ ID NO: 93

     (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 824 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Haemophilus parahaemolyticus*
       (B)   STRAIN: ATCC 10014

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

```
      TCTTAGTAGT AGCAGCAACA GACGGTCCAA TGCCACAAAC TCGTGAGCAC    50
      ATCTTATTAG GTCGCCAAGT AGGTGTTCCA TACATCATCG TATTCTTAAA    100
      CAAATGCGAT ATGGTTGACG ATGAAGAATT ATTAGAATTA GTTGAAATGG    150
      AAGTGCGTGA ACTTCTTTCA CAATATGACT TCCCAGGTGA TGACACGCCA    200
      GTAGTACGTG GTTCAGCGTT ACAAGCGTTA AACGGCGTAG CAGAGTGGGA    250
      AGAAAAAATT CTTGAATTAG CAAACCACTT AGATACATAC ATCCCAGAGC    300
      CAGAGCGTGC GATTGATAAA CCATTCTTAT TACCAATCGA AGACGTATTC    350
      TCAATCTCAG GTCGTGGTAC AGTAGTAACA GGTCGTGTTG AGCGTGGTAT    400
      CATCAAAGCG GGTGAAGAAG TTGAAATCGT AGGTATCAAA GACACTGCGA    450
      AAACAACAGT AACTGGCGTG GAAATGTTCC GTAAATTATT AGACGAAGGT    500
      CGTGCGGGTG AAAACGTTGG TGCATTATTA CGTGGTACAA AACGTGAAGA    550
      AATCGAACGT GGTCAAGTGT TAGCGAAACC AGGTACAATT ACACCACACA    600
      CAGACTTCGA ATCAGAAGTG TACGTATTAT CAAAAGAAGA AGGTGGTCGT    650
      CACACTCCAT TCTTCAAAGG TTACCGTCCA CAATTCTACT TCCGTACAAC    700
      TGACGTAACT GGTACTATTG AATTACCAGA AGGCGTAGAA ATGGTAATGC    750
      CAGGCGATAA CATCAAAATG ACAGTATCAT TAATCCACCC AATCGCGATG    800
      GACGAAGGTT TACGTTTTGC GATT                                824
```

2) INFORMATION FOR SEQ ID NO: 94

     (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 833 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:

<pre>
        (A)   ORGANISM: Haemophilus parainfluenzae
        (B)   STRAIN: ATCC 7901

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 94
</pre>

<pre>
TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC   50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCTTA CATCATCGTG   100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT   150
TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG   200
ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA   250
GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT   300
TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG   350
ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG   400
CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC   450
GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG   500
ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA   550
CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC   600
TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG   650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC   700
CGTACAACTG ACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAAT   750
GGTTATGCCT GGTGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA   800
TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG   833
</pre>

2)INFORMATION FOR SEQ ID NO: 95

        (i)SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 824 bases
            (B)   TYPE: Nucleic acid
            (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

    (ii)MOLECULE TYPE: Genomic DNA

    (vi)ORIGINAL SOURCE:
            (A)   ORGANISM: Haemophilus paraphrophilus
            (B)   STRAIN: ATCC 29241

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 95

<pre>
TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC   50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCTTA CATCATCGTA   100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT   150
TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG   200
ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA   250
GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACTTGG ATACTTACAT   300
TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG   350
ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG   400
CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC   450
GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG   500
ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAAA   550
CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC   600
TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG   650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC   700
CGTACAACTG ACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAAT   750
GGTAATGCCT GGCGATAACA TCAAAATGAC CGTATCCTTA ATCCACCCAA   800
TCGCGATGGA CCAAGGTTTA CGTT   824
</pre>

SUBSTITUTE SHEET (RULE 26)

2) INFORMATION FOR SEQ ID NO: 96

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 818 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Haemophilus segnis*
       (B)   STRAIN: ATCC 33393

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

```
GCTATCTTAG TAGTAGCAGC AACTGATGGT CCTATGCCAC AAACTCGTGA      50
GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT     100
TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA     150
ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCAG GTGATGATAC     200
TCCAATCATT CGTGGTTCTG CATTACAAGC GTTAAACGGC GTAGCAGAAT     250
GGGAAGAAAA AATCCTTGAA TTAGCTCAAG CATTAGATAC TTACATTCCT     300
GAACCTGAGC GTGCAATCGA CCAACCGTTC CTTCTTCCAA TTGAAGACGT     350
GTTCTCAATC TCTGGTCGTG GTACTGTAGT AACAGGTCGT GTAGAGCGTG     400
GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTTGGTAT CAAACCAACT     450
GCGAAAACAA CCGTAACCGG TGTTGAAATG TTCCGTAAAT TACTTGACGA     500
AGGTCGTGCA GGTGAAAACA TCGGTGCATT ATTACGTGGT ACTAAACGTG     550
AAGAAATCGA ACGTGGTCAA GTATTAGCGA AACCGGGTTC AATCACTCCA     600
CACACTGACT TCGAATCTGA AGTGTACGTA TTATCTAAAG AAGAAGGTGG     650
TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA     700
CAACTGACGT AACCGGTACT ATCGAGTTAC CGGAAGGCGT GGAAATGGTT     750
ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATCC ACCCAATCGC     800
GATGGACCAA GGTTTACG                                        818
```

2) INFORMATION FOR SEQ ID NO: 97

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 763 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Hafnia alvei*
       (B)   STRAIN: ATCC 13337

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

```
CGGCGCTATC CTGGTTGTTG CTGCGACTGA CGGCCCTATG CCTCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTW CATCATCGTR     100
TTCCTGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT     150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCWGGYGATG     200
ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGYGMACCT     250
GAGTGGGAAG CTAAGATCGT AGAACTGGCT GAAACTCTGG ATTCTTACAT     300
YCCACARCCA GAACGTGCTA TCGAYAAGCC ATTCCTGCTG CCAATCGAAG     350
```

SUBSTITUTE SHEET (RULE 26)

```
        ACGTATTCTC TATCTCTGGC CGTGGTACWG TTGTTACCGG TCGTGTAGAG        400
        CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GARATCGTTG GTATCAAAGA        450
        TACCGTTAAA TCAACTTGTA CCGGCGTTGA AATGTTCCGT AAACTGCTGG        500
        ACGAAGGTCG TGCAGGCGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG        550
    5   CGTGAAGACA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GYTCYATCAA        600
        GCCACACACC AAGTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG        650
        GCGGYCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC        700
        CGTACAACTG ACGTGACCGG TACCATCGAA TTGCCAGAAG GCGTGGAAAT        750
        GGTAATGCCA GGC                                                763
   10
```

2) INFORMATION FOR SEQ ID NO: 98

   15   (i) SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 828 bases
                (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear
   20
           (ii) MOLECULE TYPE: Genomic DNA

           (vi) ORIGINAL SOURCE:
                (A)   ORGANISM: *Kingella kingae*
   25   (B)   STRAIN: ATCC 23330

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

```
        CGGCGCAATC TTGGTATGTT CAGCAGCTGA CGGTCCTATG CCACAAACTC        50
   30   GCGAACACAT CTTGTTGGCT CGCCAAGTAG GTGTACCTTA TATCATCGTA        100
        TTCATGAACA AATGCGACAT GGTCGATGAT GCTGAGTTGT TGGAATTGGT        150
        TGAAATGGAA ATCCGTGACT TGTTGTCTAG CTACGATTTT CCAGGCGACG        200
        ATTGCCCAAT CGTTCAAGGT TCTGCATTGC GYGCATTGGA AGGCGACGCT        250
        GCATACAAAG AAAAAATCTT TGAATTGGCT GCTGCTTTGG ATAGCTACAT        300
   35   TCCTACTCCA GAACGTGCTG TTGATAAACC ATTCTTGTTG CCAATCGAAG        350
        ATGTATTCTC TATCTCTGGT CGTGGTACAG TAGTTACTGG TCGTGTAGAG        400
        CGCGGTATCA TCAAAGTAGG CGAAGAGATT GAAATCGTTG GTTTGAAAGA        450
        CACGCAAAAA ACCACTTGTA CTGGCGTGGA AATGTTCCGC AAATTGTTGG        500
        ACGAAGGTCA AGCTGGTGAT AACGTTGGTG TATTATTGCG TGGTACGAAG        550
   40   CGTGAAGACG TTGAACGTGG TCAGGTATTG GCTAAACCAG GTTCTATCAC        600
        TCCGCACACT AAATTTGAAG CTGAAGTGTA TGTGTTGAGC AAAGAAGAAG        650
        GTGGCCGTCA TACGCCATTC TTCGCTAACT ACCGCCCACA ATTCTACTTC        700
        CGTACGACTG ACGTAACTGG TGCAGTTACT TTGTCTGAGG GTGTGGAAAT        750
        GGTTATGCCA GGCGAAAACG TGAAAATCAC TGTTGAGTTG ATTGCACCTA        800
   45   TCGCTAGGAA AACGGTTTGC GTTTTGCG                                828
```

2) INFORMATION FOR SEQ ID NO: 99
   50
           (i) SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 828 bases
                (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
   55   (D)   TOPOLOGY: Linear

           (ii) MOLECULE TYPE: Genomic DNA

           (vi) ORIGINAL SOURCE:
   60   (A)   ORGANISM: *Klebsiella ornithinolytica*

```
        (B)     STRAIN: ATCC 31898

     (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 99

  5   GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG      50
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
      TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAGCTGGTT     150
      GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA     200
      CACGCCGATC GTTCGTGGTT CCGCTCTGAA AGCGCTGGAA GGCGAAGCAG     250
 10   ACTGGGAAGC GAAAATCATC GAACTGGCTG GCTACCTGGA TTCTTACATC     300
      CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA     350
      CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
      GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG     450
      ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
 15   CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCTATCAAG     600
      CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
      CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     700
      GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG     750
 20   GTCATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TTCACCCGAT     800
      CGCGATGGAC GATGGTCTGC GTTTCGCA                             828



 25  2)INFORMATION FOR SEQ ID NO: 100

        (i)SEQUENCE CHARACTERISTICS:
           (A)     LENGTH: 749 bases
           (B)     TYPE: Nucleic acid
 30        (C)     STRANDEDNESS: Double
           (D)     TOPOLOGY: Linear

      (ii)MOLECULE TYPE: Genomic DNA

 35   (vi)ORIGINAL SOURCE:
           (A)     ORGANISM: Klebsiella oxytoca
           (B)     STRAIN: ATCC 33496

     (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 100
 40
      GATGCCGCAG ACTCGTGAGC ACATCCTGCT GGGTCGTCAG GTAGGCGTTC      50
      CGTACATCAT CGTGTTCCTG AACAAGTGCG ACATGGTTGA TGACGAAGAG     100
      CTGCTGGAAC TGGTTGAAAT GGAAGTTCGT GAACTTCTGT CTCAGTACGA     150
      TTTCCCGGGC GACGACACTC CGATCGTTCG TGGTTCTGCT CTGAAAGCGC     200
 45   TGGAAGGCGA CGCWGAGTGG GAAKCKAAAA TCATCGAACT GGCTGGCTTC     250
      CTGGATTCTT ACATTCCGGA ACCAGAGCGT GCGATTGACA AGCCGTTCCT     300
      GCTGCCGATC GAAGACGTAT TCTCCATCTC CGGTCGTGGT ACCGTTGTTA     350
      CCGGTCGTGT AGAGCGCGGT ATCATCAAAG TTGGCGAAGA AGTTGAAATY     400
      GTTGGTATYA AAGACACTGC TAAGTCTACC TGTACTGGCG TTGAAATGTT     450
 50   CCGCAAACTG CTGGACGAAG CCGYGCTGG TGAGAACGTT GGTGTTCTGC     500
      TGCGTGGTAT CAAACGTGAA GAAATCGAAC GTGGTCAGGT ACTGGCTAAG     550
      CCGGGCTCTA TCAAGCCGCA CACCAAGTTC GAATCTGAAG TTTATATCCT     600
      GTCCAAAGAC GAAGGCGGCC GTCACACTCC GTTCTTCAAA GGCTACCGTC     650
      CGCAGTTCTA CTTCCGTACA ACTGACGTGA CTGGCACCAT CGAACTGCCG     700
 55   GAAGGCGTAG AGATGGTTAT GCCGGGCGAC AACATCAAAA TGGTTGTTA      749



     2)INFORMATION FOR SEQ ID NO: 101
 60
```

SUBSTITUTE SHEET (RULE 26)

```
        (i) SEQUENCE CHARACTERISTICS:
            (A)    LENGTH: 830 bases
            (B)    TYPE: Nucleic acid
            (C)    STRANDEDNESS: Double
    5       (D)    TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
    10      (A)    ORGANISM: Klebsiella planticola
            (B)    STRAIN: ATCC 33531

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

    15  TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC    50
        GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG   100
        TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT   150
        TGAAATGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG   200
        ACACTCCGAT CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA   250
    20  GACTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT   300
        CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCTATCGAAG   350
        ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG   400
        CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA   450
        TACTGCTAAR TCWACCTGTA CYGGCGTTGA AATGTTCCGC AAACTGCTGG   500
    25  ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA   550
        CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA   600
        GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG   650
        GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC   700
        CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT   750
    30  GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATTCACCCRA   800
        TCGCGATGGA CGACGGTCTG CGTTTCGCAA                          830



    35  2) INFORMATION FOR SEQ ID NO: 102

        (i) SEQUENCE CHARACTERISTICS:
            (A)    LENGTH: 806 bases
            (B)    TYPE: Nucleic acid
    40      (C)    STRANDEDNESS: Double
            (D)    TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

    45  (vi) ORIGINAL SOURCE:
            (A)    ORGANISM: Klebsiella pneumoniae subsp. ozaenae
            (B)    STRAIN: ATCC 11296

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102
    50
        CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA    50
        TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC   100
        AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TTGAGATGGA   150
        AGTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA   200
    55  TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA   250
        GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGGAACC   300
        AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT   350
        CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC   400
        ATCAAAGTAG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AAACCGCGAA   450
    60  AACCACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC   500
```

62

```
      GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA        550
      ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC        600
      CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GGCGGCCGTC        650
      ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT        700
 5    GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC        750
      GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG        800
      ACGACG                                                       806
```

10   2) INFORMATION FOR SEQ ID NO: 103

        (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 743 bases
15   (B)   TYPE: Nucleic acid
            (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA
20
        (vi) ORIGINAL SOURCE:
            (A)   ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
            (B)   STRAIN: ATCC 13883

25   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

```
      GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA         50
      TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG        100
      GAACTGGTTG AGATGGAAGT TCGTGAACTG CTGTCTCAGT ACGATTTCCC        150
30    GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG        200
      GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGCTGG CCACCTGGAT        250
      ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT CCTGCTGCC         300
      GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC        350
      GTGTAGAGCG CGGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT        400
35    ATCAAAGAAA CCGCGAAAAC CACCTGTACT GGCGTTGAAA TGTTCCGCAA        450
      ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG        500
      GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC        550
      ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGTACA TCCTGTCCAA        600
      AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT        650
40    TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC        700
      GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA             743
```

45   2) INFORMATION FOR SEQ ID NO: 104

        (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 819 bases
            (B)   TYPE: Nucleic acid
50   (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

55   (vi) ORIGINAL SOURCE:
            (A)   ORGANISM: *Klebsiella pneumoniae* subsp.
                   rhinoscleromatis
            (B)   STRAIN: ATCC 13884

60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104
                              63

```
        TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC     50
        CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA    100
        ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT GAGATGGAAG    150
   5    TTCGTGAACT RCTGTCTCAG TACGATTTCC CGGGCGACGA CACCCCGATC    200
        GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC    250
        GAAAATCATC GAACTGGCTG GCCACCTGGA TACCTATATC CCGGAACCAG    300
        AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC    350
        ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC GCGGTATCAT    400
  10    CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAA ACCGCGAAAA    450
        CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT    500
        GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT    550
        CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC CCGCACACCA    600
        AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG CGGCCGTCAC    650
  15    ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA    700
        CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG    750
        GCGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCGAT CGCGATGGAC    800
        GACGGTCTGC GTTTCGCAA                                     819
```

  20

    2) INFORMATION FOR SEQ ID NO: 105

          (i) SEQUENCE CHARACTERISTICS:
  25   (A)   LENGTH: 832 bases
                (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

  30   (ii) MOLECULE TYPE: Genomic DNA

          (vi) ORIGINAL SOURCE:
                (A)   ORGANISM: *Kluyvera ascorbata*
                (B)   STRAIN: ATCC 33433
  35
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

```
        CGGCGCGATC CTGGTTGTTG CTGCGACTGA TGGCCCTATG CCACAGACTC     50
        GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG    100
  40    TTCCTGAACA AATGYGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT    150
        TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG    200
        ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGATGCA    250
        GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT    300
        CCCAGAACCA GAACGTGCTA TCGATAAGCC GTTCCTGCTG CCAATCGAAG    350
  45    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG    400
        CGCGGTATCA TCAAAGTTGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA    450
        CACCGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG    500
        ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA    550
        CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCTATCAA    600
  50    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG    650
        GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC    700
        CGTACTACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT    750
        GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA    800
        TCGCGATGGA CGACGGCCTG CGTTTCGCAA CC                      832
```

  55

    2) INFORMATION FOR SEQ ID NO: 106

  60   (i) SEQUENCE CHARACTERISTICS:

                              64

                    (A)   LENGTH: 830 bases
                    (B)   TYPE: Nucleic acid
                    (C)   STRANDEDNESS: Double
                    (D)   TOPOLOGY: Linear
5

            (ii)MOLECULE TYPE: Genomic DNA

            (vi)ORIGINAL SOURCE:
                    (A)   ORGANISM: *Kluyvera cryocrescens*
10   (B)   STRAIN: ATCC 33435

            (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 106

          TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACTC   50
15   GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG   100
          TTCCTGAACA AATGTGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT   150
          TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG   200
          ACACTCCTAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGACGCT   250
          GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT   300
20   CCCAGAACCA GAGCGTGCGA TTGATAAGCC GTTCCTGCTG CCAATCGAAG   350
          ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG   400
          CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA   450
          CACTGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG   500
          ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA   550
25   CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCCATCAA   600
          GCCGCACACC AAATTCGAAT CTGAAGTTTA CATCCTGTCC AAAGACGAAG   650
          GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC   700
          CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT   750
          GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCAA   800
30   TCGCGATGGA CGACGGTCTG CGTTTCGCAA   830

            2)INFORMATION FOR SEQ ID NO: 107
35
              (i)SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 826 bases
                    (B)   TYPE: Nucleic acid
                    (C)   STRANDEDNESS: Double
40   (D)   TOPOLOGY: Linear

            (ii)MOLECULE TYPE: Genomic DNA

            (vi)ORIGINAL SOURCE:
45   (A)   ORGANISM: *Kluyvera georgiana*
                    (B)   STRAIN: ATCC 51603

            (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 107

50   CGCGATCCTG GTTGTTGCTG CGACTGACGG CCCGATGCCG CAGACTCGTG   50
          AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCGTACAT CATCGTGTTC   100
          CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA   150
          AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGACTTCCCG GGCGACGACA   200
          CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCTGAG   250
55   TGGAAGCGA AAATCATCGA ACTGGCGGGC TTCCTGGATT CTTACATCCC   300
          GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG   350
          TATTCTCCAT CTCCGGTCGT GGTACCGTTG TTACCGGTCG TGTAGAACGC   400
          GGTATCATCA AAGTTGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGACAC   450
          CGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG   500
60   AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT   550

```
        GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGTT CTATCAAGCC        600
        GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG        650
        GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT        700
        ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TTGAGATGGT        750
   5    AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG        800
        CGAAGGACGA AGGTCTGCGT TTCGCA                                 826
```


10   2) INFORMATION FOR SEQ ID NO: 108

          (i) SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 803 bases
              (B)   TYPE: Nucleic acid
15   (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear

          (ii) MOLECULE TYPE: Genomic DNA

20   (vi) ORIGINAL SOURCE:
              (A)   ORGANISM: *Lactobacillus casei* subsp. *casei*
              (B)   STRAIN: ATCC 393

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108
25
```
        GCTGCTGATG GCCCAATGCC ACAAACTCGT GAACATATCT TACTTTCACG         50
        TCAAGTTGGT GTTCCATACA TCGTTGTATT CATGAACAAA TGTGACATGG        100
        TTGACGATGA AGAATTACTA GAATTAGTTG AAATGGAAAT TCGTGATCTA        150
        TTAACTGAAT ATGAATTCCC TGGCGATGAC ATTCCTGTAA TCAAAGGTTC        200
   30   AGCTCTTAAA GCACTTCAAG GTGAAGCTGA CTGGGAAGCT AAAATTGACG        250
        AGTTAATGGA AGCTGTAGAT TCTTACATTC CAACTCCAGA ACGTGATACT        300
        GACAAACCAT TCATGATGCC AGTTGAGGAT GTATTCTCAA TCACTGGTCG        350
        TGGAACAGTT GCAACTGGAC GTGTTGAACG TGGACAAGTT AAAGTTGGTG        400
        ACGAAGTAGA AGTTATCGGT ATTGAAGAAG AGAGCAAAAA AGTAGTAGTA        450
   35   ACTGGAGTAG AAATGTTCCG TAAATYACTA GATTACGCTG AAGCTGGCGA        500
        CAACATTGGC GCACTTCTAC GTGGTGTTGC TCGTGAAGAT ATCCAACGTG        550
        GTCAAGTATT AGCTAAACCA GGTTCGATTA CTCCACACAC TAACTTCAAA        600
        GCTGAAACTT ATGTTTTAAC TAAAGAAGAA GGTGGACGTC ACACTCCATT        650
        CTTCAACAAC TACCGCCCAC AATTCTATTT CCGTACTACT GACGTAACTG        700
   40   GTATTGTTAC ACTTCCAGAA GGTACTGAAA TGGTAATGCC TGGTGATAAC        750
        ATTGAGCTTG CAGTTGANCT AATTGCACCA ATCGCTATCG AAGACGGTAC        800
        TAA                                                          803
```


45   2) INFORMATION FOR SEQ ID NO: 109

          (i) SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 825 bases
              (B)   TYPE: Nucleic acid
50   (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear

          (ii) MOLECULE TYPE: Genomic DNA
55
          (vi) ORIGINAL SOURCE:
              (A)   ORGANISM: *Lactococcus lactis* subsp. *lactis*
              (B)   STRAIN: ATCC 19435

60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

                                    66

                      SUBSTITUTE SHEET (RULE 26)

```
        CGGTGCAATC CTCGTTGTTG CTGCAACTGA TGGACCAATG CCACAAACTC          50
        GTGAACACAT CTTGCTTTCA CGTCAAGTTG GTGTTAAATA CCTTATCGTC         100
        TTCCTTAACA AGGCTGACCT TGTTGATGAT GAAGAATTGA TGGAACTCGT         150
    5   TGAAATGGAA GTTCGTGACC TCTTGAGCGA ATACGACTTC CCAGGTGACG         200
        ATATTCCTGT AATCGCTGGT TCAGCACTTG GTGCTTTGAA CGGTGAACCA         250
        CAATGGGTTG CTAAAGTTGA AGAATTGATG GACATCGTTG ATGAATACAT         300
        CCCAACTCCA GAACGCGACA CTGACAAACC ACTCCTTCTT CCAGTCGAAG         350
        ACGTATTCTC TATCACTGGT CGTGGTACAG TTGCTTCAGG ACGTATCGAA         400
   10   CGTGGTACTG TTAAAGTTGG TGACGAAGTT GAAATCGTTG GTATCAAAGA         450
        AGAAACTAAA AAAGCTGTTG TTACTGGTAT CGAAATGTTC CGTAAAACAC         500
        TTACTGAAGG TCTTGCTGGT GATAACGTCG GTGCACTTCT CCGTGGTATC         550
        CAACGTGACG AAATCGAACG TGGTCAAGTT ATTGCTAAAC CAGGTTCAAT         600
        CACTCCACAC AAACTTTTCG AAGGTGAAGT TTACGTATTG AGCAAAGAAG         650
   15   AAGGCGGACG TCACACTCCA TTCTTCGACA ACTACCGTCC TCAATTCTAC         700
        TTCCACACAA CTGACGTTAC TGGTTCAGTT AAACTTCCAG AAGGAACTGA         750
        AATGGTAATG CCTGGTGACA ACGTGCATAT CGACGTTGAA TTGATCCACC         800
        CAGTTGCGAT CGAACAAGGT ACTAC                                     825
```

20

2) INFORMATION FOR SEQ ID NO: 110

    (i) SEQUENCE CHARACTERISTICS:
25   (A)   LENGTH: 824 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

30   (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Leclercia adecarboxylata*
        (B)   STRAIN: ATCC 23216
35

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

```
        GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCAATGC CTCAGACCCG          50
        TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTTC ATCATCGTGT         100
   40   TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT         150
        GAGATGGAAG TTCGTGAACT YCTGTCCCAG TACGACTTCC CGGGCGACGA         200
        CACCCCAATC GTTCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG         250
        AGTGGGAAGA GAAAATCATC GARCTGGCTG GCTACCTGGA TTCCTACATC         300
        CCAGAGCCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA         350
        CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC         400
   45   GCGGTATCAT CAARGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAGGAC         450
        ACTGCTAAGT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA         500
        CGAAGGCCGT GCCGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC         550
        GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CTAAGCCAGG CTCYATCAAG         600
        CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCYA AAGACGAAGG         650
   50   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC         700
        GTACKACTGA CGTGACCGGT ACCATCGARC TGCCAGAAGG CGTTGAGATG         750
        GTAATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT         800
        CGCAATGGAC GATGGTCTGC GTTC                                      824
```

55

2) INFORMATION FOR SEQ ID NO: 111

60   (i) SEQUENCE CHARACTERISTICS:

                (A)   LENGTH: 838 bases
                (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

        (ii)MOLECULE TYPE: Genomic DNA

        (vi)ORIGINAL SOURCE:
                (A)   ORGANISM: *Legionella micdadei*
                (B)   STRAIN: ATCC 33218

        (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 111

```
CGGAGCGATA TTAGTAGTAT CAGCAGCGGA TGGCCCAATG CCTCAAACGA      50
GAGAGCACAT ACTYTTATCC CGSCAGGTAG GTGTTCCCTA TATAGTAGTG     100
TTCTTAAACA AAGCTGACAT GGTGGATGAT GCGGAGTTAT TAGAATTAGT     150
TGAAATGGAA GTACGCGAYT TGTTGAGCAG CTATGAATTT CCAGGAGATG     200
AGATCCCGAT TGTAGTTGGT TCAGCATTAA AAGCATTGGA AGGCGATACG     250
AGTGATATAG GTGTACCAGC GATTGAGAAG TTAGTTGAGA CGATGGATTC     300
TTATATACCT GAGCCGGTAA GAAACATCGA TAAAAGTTTC TTGTTACCGA     350
TCGAAGACGT GTTCTCAATA TCTGGACGAG GAACAGTAGT AACAGGACGT     400
ATCGAAAGCG GGATCATCAA AGTTGGTGAG GAAGTCGAGA TTGTTGGTAT     450
ACGTGACACT CAAAAGACGA CATGCACAGG CGTTGAAATG TTCCGTAAAT     500
TACTTGACGA AGGTCGAGCT GGAGACAACG TTGGTATATT GCTACGTGGT     550
ACGAAGCGGG ATGAAGTTGA ACGCGGACAA GTATTAGCTA AGCCGGGAAG     600
CATTAAACCG CATACTAAAT TTGAAGCTGA AGTGTATGTG TTGTCAAAAG     650
ATGAAGGTGG ACGTCATACC CCATTCTTTA ACGGATATCG GCCTCAATTT     700
TACTTCAGGA CCACAGACGT AACTGGTTCT TGTGATTTAC CTGARGGTAT     750
AGAAATGGTA ATGCCAGGTG ATAACGTCAA GCTGATTGTT AGCTTACACT     800
CACCGATTGC TATGGACGAA GGTTTGCGTT TTGCAATC                  838
```

    2)INFORMATION FOR SEQ ID NO: 112

        (i)SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 838 bases
                (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

        (ii)MOLECULE TYPE: Genomic DNA

        (vi)ORIGINAL SOURCE:
                (A)   ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
                (B)   STRAIN: ATCC 33152

        (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 112

```
CGGAGCGATA CTGGTTGTAT CAGCAGCTGA TGGTCCTATG CCACAAACGA      50
GGGAACACAT TCTATTGTCT CGCCAGGTAG GTGTTCCATA TATTGTTGTG     100
TTCATGAACA AAGCGGATAT GGTTGATGAC CCTGAGTTAT TAGAGTTAGT     150
GGAAATGGAA GTGCGAGATT TATTAAGCAG TTACGATTTC CCAGGGGATG     200
ACATACCTAT TGTTGTTGGT TCAGCTTTGA AAGCATTGGA AGGTGAAGAC     250
AGTGATATAG GCGTTAAGGC TATTGAGAAA TTGGTTGAAA CAATGGATTC     300
ATACATTCCT GAGCCAGTTA GAAACATAGA CAAGCCATTT TTGTTGCCGA     350
TTGAAGACGT ATTTTCAATT TCTGGACGCG GAACAGTGGT AACTGGTCGT     400
GTAGAGAGTG GAATTGTTAA AGTTGGTGAG GAAGTTGAAA TTGTTGGAAT     450
AAGAGACACC CAAAAGACGA CTTGTACGGG TGTTGAGATG TTCCGTAAAT     500
TACTTGATGA AGGTCGAGCT GGTGATAACG TTGGTGTGTT ATTACGAGGT     550
```

                                68
```

```
          ACGAAGCGAG ATGAAGTGGA GCGTGGACAG GTATTGGCGA AGCCAGGAAC        600
          CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG        650
          AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATACCG TCCACAATTC        700
          TATTTCAGAA CCACTGACGT GACAGGTACT TGTGACTTGC CATCAGGAGT        750
    5     TGAAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG        800
          CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT                    838
```


    10   2)INFORMATION FOR SEQ ID NO: 113

             (i)SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 828 bases
                (B)   TYPE: Nucleic acid
    15   (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

          (ii)MOLECULE TYPE: Genomic DNA

    20   (vi)ORIGINAL SOURCE:
                (A)   ORGANISM: *Leminorella grimontii*
                (B)   STRAIN: ATCC 33999

          (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 113
    25

```
          GTGCAATCCT GGTAGTAGCA GCGACTGACG GCCCGATGCC TCAGACTCGC         50
          GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA TCATCGTATT        100
          CCTGAACAAG TGCGATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG        150
          ARATGGAAGT TCGCGAACTG CTGTCTCAGT ACGACTTCCC GGGCGACGAC        200
    30    ACTCCGGTAG TCCGCGGTTC AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA        250
          GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC        300
          CAGAACCTGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC KATCGAAGAC        350
          GTATTCTCTA TCTCCGGCCG TGGTACCGTT GTTACCGGTC GTGTAGAGCG        400
          CGGCATCATC AAAGTCGGTG AAGAAGTGGA AATCGTCGGT ATCAAAGATA        450
    35    CCACCAAGAC CACCTGTACC GGCGTTGAAA TGTTCCGTAA GCTGCTGGAC        500
          GAAGGCCGTG CGGGCGAGAA CGTGGGCGTT CTGCTGCGCG GTACCAAGCG        550
          TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC        600
          CTCACACCCA GTTCGTGTCA GAAGTGTATA TCCTGAGCAA GGATGAAGGC        650
          GGCCGTCATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG        700
    40    TACGACTGAC GTGACAGGCA CCATCGAACT GCCGGAAGGC GTAGAGATGG        750
          TAATGCCAGG CGACAACATT CAGATGACCG TAAGTCTGAT TGCGCCGATC        800
          GCAATGGACG AAGGTCTGCG CTTCGCAA                               828
```


    45
          2)INFORMATION FOR SEQ ID NO: 114

             (i)SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 826 bases
    50   (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

          (ii)MOLECULE TYPE: Genomic DNA
    55
          (vi)ORIGINAL SOURCE:
                (A)   ORGANISM: *Leminorella richardii*
                (B)   STRAIN: ATCC 33998

    60   (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 114

                                69

SUBSTITUTE SHEET (RULE 26)

```
      GCTATCCTGG TTGTTGCTGC GACTGACGGC CCAATGCCTC AGACTCGTGA        50
      GCACATCCTG CTGGGTCGCC AGGTAGGCGT TCCTTACATC ATCGTGTTCC       100
      TGAACAAGTG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA       150
   5  ATGGAAGTTC GTGAACTTCT GTCTCAATAC GACTTCCCGG GCGACGATAC       200
      GCCGGTTGTT CGCGGTTCAG CGCTGAAAGC GCTGGAAGGT GACGCYGAGT       250
      GGGAARCGAA AATCATTGAA CTGGCGGAAT CCTTRGATAC TTAYATTCCA       300
      GAGCCAGAGC GTGCGATTGA CAAGCCGTTC CTGCTGCCTA TCGAAGACGT       350
      TTTCTCTATC TCTGGCCGTG GTACTGTAGT CACCGGTCGT GTAGAGCGCG       400
  10  GCATCATCAA AGTTGGTGAA GAAGTGGAAA TCGTGGGAAT CAAAGACACC       450
      ACCAAGACCA CCTGTACTGG CGTTGAAATG TTCCGTAAGC TGCTGGACGA       500
      AGGCCGTGCA GGTGAGAACG TTGGTGTTCT GCTGCGYGGT ACTAAGCGTG       550
      ACGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCAGGCAC CATCACTCCT       600
      CACACAGAAT TCGTGTCAGA AGTGTATATC CTGAGCAAGG ATGAAGGCGG       650
  15  YCGTCATACT CCGTTCTTCA AAGGCTACCG TCCTCAGTTC TACTTCCGTA       700
      CGACTGACGT GACCGGCACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA       750
      ATGCCAGGCG ATAACATCCA GATGGTAGTT ACGCTGATTG CCCCAATCGC       800
      GATGGACGAA GGTCTGCGCT TCGCAA                                 826
```

  20

  2) INFORMATION FOR SEQ ID NO: 115

         (i) SEQUENCE CHARACTERISTICS:
  25   (A)   LENGTH: 843 bases
              (B)   TYPE: Nucleic acid
              (C)   STRANDEDNESS: Double
              (D)   TOPOLOGY: Linear

  30   (ii) MOLECULE TYPE: Genomic DNA

         (vi) ORIGINAL SOURCE:
              (A)   ORGANISM: *Leptospira interrogans*
              (B)   STRAIN: ATCC 23581
  35
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

```
      TGCGGCGATT CTTGTAGTAT CCGCAACTGA CGGACCTATG CCACAAACAA        50
      AAGAACATAT CCTTCTTGCT CGTCAGGTAG GTGTTCCATA TGTAATTGTA       100
  40  TTCATTAACA AAGCAGATAT GCTTGCTGCT GACGAAAGAG CAGAAATGAT       150
      CGAAATGGTT GAGATGGACG TTCGTGAACT TCTCAATAAG TATAGCTTCC       200
      CAGGAGATAC AACTCCTATC GTTCATGGTT CTGCGGTAAA AGCACTTGAG       250
      GGCGATGAAT CTGAAATTGG GATGCCTGCA ATTCTCAAAT TGATGGAAGC       300
      TCTGGATACT TTCGTTCCAA ATCCAAAACG TGTAATCGAC AAACCTTTCC       350
  45  TTATGCCAGT AGAAGACGTT TTCTCGATCA CTGGTCGTGG AACTGTTGCA       400
      ACTGGAAGAG TGGAACAAGG TGTTTTGAAA GTGAACGACG AAGTTGAAAT       450
      TATCGGTATC CGCCCAACAA CAAAAACTGT TGTTACCGGT ATCGAAATGT       500
      TCAGAAAACT TCTCGATCAA GCGGAAGCTG GCGACAACAT CGGCGCTCTT       550
      CTTCGTGGAA CTAAAAAAGA AGAAATCGAA AGAGGGCAAG TTCTTGCGAA       600
  50  GCCAGGTTCT ATCACTCCTC ACAAAAAGTT TGCCGCTGAG GTGTATGTAT       650
      TAACTAAGGA TGAAGGCGGA CGTCATACTC CGTTTATCAA TAACTACCGT       700
      CCTCAGTTTT ACTTTAGAAC AACTGACGTA ACCGGAGTTT GTAACCTTCC       750
      TAATGGTGTC GAAATGGTTA TGCCTGGTGA TAACGTTTCT TTGACGGTTG       800
      AATTGATTAG CCCGATCGCA ATGGACAAGG GTCTTAAGTT CGC             843
```

  55

  2) INFORMATION FOR SEQ ID NO: 116

  60   (i) SEQUENCE CHARACTERISTICS:

```
        (A)    LENGTH: 832 bases
        (B)    TYPE: Nucleic acid
        (C)    STRANDEDNESS: Double
        (D)    TOPOLOGY: Linear
 5

    (ii)MOLECULE TYPE: Genomic DNA

    (vi)ORIGINAL SOURCE:
        (A)    ORGANISM: Megamonas hypermegale
10      (B)    STRAIN: ATCC 25560

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 116

     CGGTGCTATC CTCGTTGTTA GTGCTGCTGA TGGTCCTATG CCTCAGACTC    50
15   GTGAACACAT CCTTCTCGCT CGTCAGGTTG GTGTTCCAGC TATCGTTGTA    100
     TTCCTCAACA AAGCTGACCA GGTTGATGAC CCTGAACTTC TCGAACTTGT    150
     TGAAATGGAA GTTCGTGAAC TTCTTTCCAG CTATGACTTC CCAGGCGATG    200
     ACGTTCCAGT AATCACTGGT TCCGCTCTTC AGGCTCTCGA AGGCGACGAA    250
     GAAGCTAAAA AGAAAATTCT TGAATTAATG GATGCTGTTG ATGATTACAT    300
20   CCCAACTCCA ACACGTGACA CTGATAAACC TTTCTTAATG CCAGTTGAAG    350
     ACGTATTCAC AATTACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA    400
     CGTGGCGAAC TTAAACTTGG TGACAGCGTT GAAATCGTTG GTCTTTCCGA    450
     TGAAAAGAAA TCCACTACTG TAACTGGTAT CGAAATGTTC CGCAAAATGC    500
     TTGATAGCGC TGTTGCTGGT GATAACATCG GTGCACTTCT TCGTGGTATT    550
25   GACCGTAAAG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CTGGCACAAT    600
     TCATCCACAC AAAAAATTCA AAGCTCAGGT TTACGTATTA ACTAAAGAAG    650
     AAGGTGGACG TCATACTCCA TTCTTCTCCA ACTATCGTCC ACAGTTCTAT    700
     TTCCGTACTA CTGACGTTAC TGGTGTTGTA ACTCTTCCAG AAGGTACTGA    750
     AATGGTTATG CCTGGCGATA ACATTGAAAT GAGCATCGAA CTCATCACTC    800
30   CAATCGCTAT TGAAAAAGGT CTTCGCTTCG CT                       832




    2)INFORMATION FOR SEQ ID NO: 117
35
        (i)SEQUENCE CHARACTERISTICS:
        (A)    LENGTH: 820 bases
        (B)    TYPE: Nucleic acid
        (C)    STRANDEDNESS: Double
40      (D)    TOPOLOGY: Linear


    (ii)MOLECULE TYPE: Genomic DNA

    (vi)ORIGINAL SOURCE:
45      (A)    ORGANISM: Mitsuokella multacida
        (B)    STRAIN: ATCC 27723

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 117

50   TGGTGCTATC CTCGTCGTTT CCGCTGCTGA TGGCCCGATG CCGCAGACGC    50
     GTGAGCACAT CCTGCTCGCT CGCCAGGTCG GTGTTCCGGC AATCGTTGTC    100
     TTCCTCAACA AGGTTGACCA GGTTGACGAT CCGGAGCTCC TCGAGCTCGT    150
     CGAGATGGAA GTTCGCGAGC TGCTCTCCAG CTACGACTTC CCGGGCGATG    200
     ACATCCCTGT AATCGCTGGT TCCGCTCTGA AGGCCCTCGA AGGCGACGAA    250
55   GAGCAGAAGA AGAACATCCT CAAGCTCATG GAAGCTGTCG ATGAGTACAT    300
     CCCGACGCCG GTCCGCGACA ACGCTAAGCC GTTCCTGATG CCGGTCGAGG    350
     ATGTCTTCAC GATCACGGGC CGTGGTACGG TTGCAACGGG CCGCGTTGAG    400
     CGTGGTGAGC TCAAGATGAA CGATACGGTT GAGATCGTTG GTCTGCAGGA    450
     CGAGCCGCGT CAGACGGTTG TCACGGGCAT CGAGATGTTC CGCAAGATGC    500
60   TTGATTTCGC TGAGGCTGGC GATAACATCG GTGCTCTGCT CCGTGGTATC    550
```

```
         GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT        600
         TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG        650
         AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC        700
         TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAACTGCCGG AAGGCACGGA        750
    5    GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC        800
         CGATCGCTAT CGAGAAGGGC                                        820
```

    10   2) INFORMATION FOR SEQ ID NO: 118

             (i) SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 831 bases
                 (B)   TYPE: Nucleic acid
    15   (C)   STRANDEDNESS: Double
                 (D)   TOPOLOGY: Linear

         (ii) MOLECULE TYPE: Genomic DNA

    20   (vi) ORIGINAL SOURCE:
                 (A)   ORGANISM: *Mobiluncus curtisii* subsp. *holmesii*
                 (B)   STRAIN: ATCC 35242

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118
    25

```
         CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA         50
         AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC        100
         GCTCTGAACA AGTGCGATTC TTCCGATGTG GACGAAGACA TGCTCGAAAT        150
         CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG        200
    30   ACTGCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC        250
         GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTCG ATACCTACAT        300
         TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG        350
         ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA        400
         CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTCGTCC        450
    35   TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG        500
         ACGAAGCCTA CGCCGGCGAG AACTGTGGTC TGTTGCTGCG TGGCACCAAG        550
         CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCCTG GCTCCGTGAC        600
         CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG        650
         GTGGACGTCA CAAGTCGTTC TACGACGGCT ACCGCCCGCA GTTCTTCTTC        700
    40   CGCACCACCG ACGTGACCGG TGTTATTCAC CTGCCCGAAG GCACCGAAAT        750
         GGTTATGCCT GGCGACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA        800
         TCGCTATGGA GGAAGGTCTC GGCTTCGCTA T                         831
```

    45
         2) INFORMATION FOR SEQ ID NO: 119

             (i) SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 825 bases
    50   (B)   TYPE: Nucleic acid
                 (C)   STRANDEDNESS: Double
                 (D)   TOPOLOGY: Linear

         (ii) MOLECULE TYPE: Genomic DNA

    55
         (vi) ORIGINAL SOURCE:
                 (A)   ORGANISM: *Moellerella wisconsensis*
                 (B)   STRAIN: ATCC 35017

    60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

```
      GGTGCAATTC TGGTTGTTGC TGCAACTGAT GGCCCTATGC CACAGACTCG        50
      TGAGCACATC CTGTTAGGTC GTCAGGTTGG CGTTCCATAC ATCATCGTTT       100
      TCCTGAACAA ATGTGACATG GTAGACGACG AAGAGCTGTT AGAACTGGTT       150
 5    GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGATTTCC CAGGCGATGA       200
      CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCTCTGGAA GGCGAAGCTG       250
      AGTGGGAAGC TAAAATCATT GAACTGGCAG AAGCACTGGA TTCTTATATC       300
      CCAGAGCCAG AGCGTGACAT TGATAAGCCA TTCCTGTTAC CAATCGAAGA       350
      CGTATTCTCA ATTTCAGGCC GTGGTACAGT TGTTACTGGT CGTGTTGAGC       400
 10   GTGGTATCGT TAAAGTCGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT       450
      ACCGTGAAAA CAACATGTAC TGGCGTTGAA ATGTTCCGTA AACTGCTGGA       500
      CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAAC       550
      GTGATGATAT CGAACGTGGT CAAGTATTGG CTAAACCAGG TTCAATCACT       600
      CCGCATACAA CTTTCGAATC AGAAGTTTAC ATCCTGAGCA AAGATGAAGG       650
 15   TGGCCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAG TTCTACTTCC       700
      GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG       750
      GTAATGCCAG GTGATAACAT CAAAATGATC GTTACTCTGA TCCACCCAAT       800
      TGCAATGGAT GCAGGTCTGC GTTTT                                  825
```

20

2) INFORMATION FOR SEQ ID NO:120

    (i) SEQUENCE CHARACTERISTICS:
25
        (A)   LENGTH: 827 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

30   (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Branhamella catarrhalis*
        (B)   STRAIN: ATCC 43628
35
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

```
      TGGTGCTATC TTGGTTGTTT CTGCAACTGA TGGTCCTATG CCACAAACTC        50
      GTGAGCATAT CCTACTATCT CGTCAGGTTG GTGTACCATA CATCATGGTA       100
 40   TTCATGAACA AGTGCGATAT GGTTGATGAT GAAGAGCTAC TAGAATTGGT       150
      TGAAATGGAA GTTCGTGAAC TTCTATCTGA CTATGATTTC CCTGGTGATG       200
      ATACCCCAAT CATCAAAGGT TCAGCACTAG AAGCATTGAA TGGTTCTGAT       250
      GGTAAATATG GCGAGCCTGC AGTTCTAGAA CTGCTAGACA CACTAGACAG       300
      CTATATCCCA GAGCCTGAGC GTGATATCGA TAAGTCATTC TTGATGCCAA       350
 45   TTGAAGATGT CTTCTCGATC TCAGGTCGTG GTACAGTTGT GACTGGTCGT       400
      GTTGAATCAG GTATTATTAA AGTTGGTGAT GAAATTGAAA TCATCGGTAT       450
      CAAACCAACT GCTAAAACCA CCTGTACTGG TGTTGAAATG TTCCGTAAAC       500
      TGTTAGACGA AGGTCGTGCA GGTGAGAACT GTGGTATCTT GTTGCGTGGT       550
      ACTAAGCGTG AAGAAGTTCA ACGCGGTCAA GTACTTGCAA AACCAGGTTC       600
 50   AATCACCCCA CATACTAAGT TTGATGCTGA AGTTTATGTA CTGTCAAAAG       650
      AAGAAGGTGG TCGTCACACC CCATTCTTAA ATGGCTATCG CCCACAGTTC       700
      TACTTCCGTA CCACAGATGT GACTGGTGCC ATCACTCTAC AAGAAGGTAC       750
      CGAAATGGTT ATGCCTGGTG ACAATGTTGA GATGAGTGTT GAGCTTATCC       800
      ACCCAATCGC CAGGATAAAG GTCTACG                               827
```

55

2) INFORMATION FOR SEQ ID NO: 121

60   (i) SEQUENCE CHARACTERISTICS:

```
        (A)    LENGTH: 806 bases
        (B)    TYPE: Nucleic acid
        (C)    STRANDEDNESS: Double
        (D)    TOPOLOGY: Linear
5
    (ii)MOLECULE TYPE: Genomic DNA

    (vi)ORIGINAL SOURCE:
        (A)    ORGANISM: Morganella morganii subsp. morganii
10      (B)    STRAIN: ATCC 25830

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 121
```

```
     CGGCGCTATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACCC      50
15   GTGAGCACAT CCTGTTAGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA     100
     TTCCTGAACA AATGTGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT     150
     TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCTGGCGACG     200
     ACACGCCAAT CGTTCGCGGT TCAGCGCTGA AAGCACTGGA AGGCGAGCCA     250
     GAGTGGGAAG CTAARATCGT TGAACTGGCA GGTTTCCTGG ATTCTTACAT     300
20   CCCTGAGCCA GAGCGTGCAA TTGACAAGCC GTTCCTGCTG CCAATCGAAG     350
     ACGTATTCTC AATCTCCGGC CGTGGTACCG TTGTTACCGG TCGTGTTGAG     400
     CGCGGTATCA TCAAGGTTGG TGAGGAAGTT GAAATCGTGG GTATCAAAGA     450
     TACTGCGAAA ACCACCTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG     500
     ACGAAGGCCG TGCMGGTGAG AACGTCGGTG TTCTGCTGCG TGGTACCAAG     550
25   CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GTTCAATCAA     600
     ACCACAYACC AAATTTGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG     650
     GTGGTCGTCA TACTCCATTC TTCAAAGGYT ACCGTCCACA GTTCTACTTC      700
     CGTACCACAG ACGTAACAGG TACTATCGAA CTGCCGGAAG GCGTTGAAAT     750
     GGTAATGCCG GGCGACAACA TCAAAATGAT CGTCACCCTG ATCCACCCAA     800
30   TCGCAA                                                     806
```

```
    2)INFORMATION FOR SEQ ID NO: 122
35
        (i)SEQUENCE CHARACTERISTICS:
        (A)    LENGTH: 825 bases
        (B)    TYPE: Nucleic acid
        (C)    STRANDEDNESS: Double
40      (D)    TOPOLOGY: Linear

    (ii)MOLECULE TYPE: Genomic DNA

    (vi)ORIGINAL SOURCE:
45      (A)    ORGANISM: Mycobacterium tuberculosis
        (B)    STRAIN: TB 299

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 122
```

```
50   GGTGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCGATGC CCCAGACCCG      50
     CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC ATCCTGGTAG     100
     CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC     150
     GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC     200
     CCCGGTTGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT     250
55   GGGTTGCCTC TGTCGAGGAA CTGATGAACG CGGTCGACGA GTCGATTCCG     300
     GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCGG TCGAGGACGT     350
     CTTCACCATT ACCGGCCGCG GAACCGTGGT CACCGGACGT GTGGAGCGCG     400
     GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG     450
     ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA     500
60   CCAGGGCCAG GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GGCGTCAAGC     550
```

74

```
        GCGAGGACGT CGAGCGTGGC CAGGTTGTCA CCAAGCCCGG CACCACCACG      600
        CCGCACACCG AGTTCGAAGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG      650
        CGGCCGGCAC ACGCCGTTCT TCAACAACTA CCGTCCGCAG TTCTACTTCC      700
        GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG      750
     5  GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT      800
        CGCCATGGAC GAAGGTCTGC GTTTC                                825
```

   10   2) INFORMATION FOR SEQ ID NO: 123

            (i) SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 806 bases
                (B)   TYPE: Nucleic acid
   15   (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

         (ii) MOLECULE TYPE: Genomic DNA

   20   (vi) ORIGINAL SOURCE:
                (A)   ORGANISM: *Neisseria cinerea*
                (B)   STRAIN: ATCC 14685

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123
   25

```
        CGGTGCGATC TTGGTATGTT CCGCAGCTGA CGGTCCTATG CCGCAAACTC       50
        GCGAACACAT CCTGTTGGCC CGCCAAGTAG GTGTACCTTA CATCATCGTG      100
        TTCATGAACA AATGCGACAT GGTTGACGAT GCCGAGCTGT TGGAGCTGGT      150
        TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGTGACG      200
   30   ACTGCCCGAT CGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGACGCA      250
        GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT      300
        CCCAACACCT GAGCGTGCAG TGGACAAACC TTTCTTGTTG CCTATCGAAG      350
        ACGTATTCTC TATTTCCGGT CGCGGTACAG TAGTAACCGG TCGTGTAGAG      400
        CGCGGTATCA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA      450
   35   AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG      500
        ACGAAGGTCA AGCTGGTGAC AACGTAGGTG TATTGCTGCG TGGTACTAAA      550
        CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACTATCAC      600
        TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG      650
        GTGGTCGTCA CACTCCGTTC TTCGCTAACT ACCGTCCACA ATTCTACTTC      700
   40   CGTACTACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTAGAAAT      750
        GGTAATGCCG GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA      800
        TCGCTA                                                     806
```

   45
        2) INFORMATION FOR SEQ ID NO: 124

            (i) SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 822 bases
   50   (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

         (ii) MOLECULE TYPE: Genomic DNA
   55
         (vi) ORIGINAL SOURCE:
                (A)   ORGANISM: *Neisseria elongata* subsp. *elongata*
                (B)   STRAIN: ATCC 25295

   60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

```
      CGGCGCAATC TTGGTATGTT CCGCTGCYGA CGGTCCTATG CCGCAAACTC        50
      GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG       100
      TTCATGAATA AATGCGACAT GGTTGAYGAT GCCGAACTGC TGGAACTGGT       150
  5   TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG       200
      ACTGCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGACGCA       250
      GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT       300
      CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG       350
      ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG       400
 10   CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA       450
      AACCCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG       500
      ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA       550
      CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC       600
      TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG       650
 15   GTGGTCGTCA TACTCCGTTC TTCGCTAACT ACCGTCCACA ATTCTACTTC       700
      CGTACTACCG ACGTAACCGG TGCGGTTACT TTGGAAGAAG GTGTAGAAAT       750
      GGTTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAACTG ATTGCACCTA       800
      TCGCTATGGA AGAAGGTCTG CG                                     822
```

20

2) INFORMATION FOR SEQ ID NO: 125

    (i) SEQUENCE CHARACTERISTICS:
25   (A)   LENGTH: 820 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

30   (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Neisseria flavescens*
        (B)   STRAIN: ATCC 13120
35
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

```
      CGGCGCGACT TGGTATGTTC CGCAGCTGAC GGTCCTATGC CGCAAACCCG        50
      CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT       100
 40   TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAACTGGTT       150
      GAAATGGAAA TTCGTGACTT GTTGTCAAGC TACGACTTCC CAGGCGACGA       200
      CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG       250
      CTTACGAAGA AAAAATCTTC GAATTGGCTG CTGCCTTGGA CAGCTACATC       300
      CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA       350
 45   CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC       400
      GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA       450
      ACTCAAAAAA CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA       500
      CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC       550
      GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT       600
 50   CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG       650
      TGGTCGTCAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC       700
      GTACTACCGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG       750
      GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCAAT       800
      CGCTATGGAA GAAGTCTGCG                                        820
```

55

2) INFORMATION FOR SEQ ID NO: 126

60   (i) SEQUENCE CHARACTERISTICS:

```
        (A)     LENGTH: 830 bases
        (B)     TYPE: Nucleic acid
        (C)     STRANDEDNESS: Double
        (D)     TOPOLOGY: Linear
 5
    (ii)MOLECULE TYPE: Genomic DNA

    (vi)ORIGINAL SOURCE:
        (A)     ORGANISM: Neisseria gonorrhoeae
10      (B)     STRAIN: ATCC 49226

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 126

    GGTGCAATCC TGGTATGTTC TGCTGCCGAC GGCCCTATGC CGCAAACCCG     50
15  CGAACACATC CTGCTGGCCC GTCAAGTAGG CGTACCTTAC ATCATCGTGT    100
    TCATGAACAA ATGCGACATG GTCGACGATG CCGAGCTGTT GGAACTGGTT    150
    GAAATGGAAA TCCGCGACCT GCTGTCCAGC TACGACTTCC CCGGCGACGA    200
    CTGCCCGATC GTACAAGGTT CCGCACTGAA AGCCTTGGAA GGCGATGCCG    250
    CTTACGAAGA AAAAATCTTC GAACTGGCTA CCGCATTGGA CAGCTACATC    300
20  CCGACTCCCG AGCGTGCCGT GGACAAACCA TTCCTGCTGC CTATCGAAGA    350
    CGTGTTCTCC ATTTCCGGCC GCGGTACCGT AGTCACCGGC CGTGTAGAGC    400
    GAGGTATCAT CCACGTTGGT GACGAGATTG AAATCGTCGG TCTGAAAGAA    450
    ACCCAAAAAA CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA    500
    CGAAGGTCAG GCGGGCGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC    550
25  GTGAAGACGT AGAACGCGGT CAGGTATTGG CCAAACCGGG TACTATCACT    600
    CCTCACACCA AGTTCAAAGC AGAAGTGTAC GTATTGAGCA AAGAAGAGGG    650
    CGGCCGCCAT ACCCCGTTTT TCGCCAACTA CCGTCCCCAA TTCTACTTCC    700
    GTACCACTGA CGTAACCGGC GCGGTTACTT TGGAAAAAGG TGTGGAAATG    750
    GTAATGCCGG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT    800
30  CGCTATGGAA GAAGGTCTGC GCTTTGCGAT                          830


    2)INFORMATION FOR SEQ ID NO: 127
35
        (i)SEQUENCE CHARACTERISTICS:
        (A)     LENGTH: 816 bases
        (B)     TYPE: Nucleic acid
        (C)     STRANDEDNESS: Double
40      (D)     TOPOLOGY: Linear

    (ii)MOLECULE TYPE: Genomic DNA

    (vi)ORIGINAL SOURCE:
45      (A)     ORGANISM: Neisseria lactamica
        (B)     STRAIN: ATCC 23970

    (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 127

50  CGGCGCAATC TTGGTATGTT CCGCCGCCGA CGGCCCTATG CCGCAAACCC     50
    GCGAACACAT TCTGTTGGCC CGCCAAGTAG GTGTACCTTA CATCATCGTA    100
    TTCATGAACA AATGCGATAT GGTCGACGAT GCCGAGCTGT TGGAACTGGT    150
    TGAAATGGAA ATCCGCGACC TGCTGTCAAG CTACGACTTC CCAGGCGACG    200
    ACTGCCCAAT CGTACAAGGT TCCGCACTGA AAGCTTTGGA AGGCGATGCC    250
55  GCTTACGAAG AAAAAATCTT CGAACTGGCT GCCGCATTGG ACAGCTACAT    300
    CCCGACTCCC GAGCGTGCCG TGGACAAACC GTTCCTGCTG CCTATCGAAG    350
    ACGTATTCTC CATCTCCGGC CGCGGTACGG TAGTAACCGG CCGTGTAGAG    400
    CGCGGTGTCA TCCACGTTGG CGACGAGATC GAAATCGTCG GTCTGAAAGA    450
    AACCCAAAAA ACCACCTGTA CCGGTGTCGA GATGTTCCGC AAACTGCTGG    500
60  ACGAAGGTCA GGCAGGCGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA    550
```

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```
         CGTGAAGAAG  TGGAACGCGG  TCAGGTATTA  GCCAAACCGG  GTACCATCAC        600
         TCCGCACACC  AAGTTCAAAG  CAGAAGTGTA  TGTATTGAGC  AAAGAAGAGG        650
         GCGGTCGTCA  CACTCCGTTC  TTCGCCAACT  ACCGTCCGCA  ATTCTACTTC        700
         CGTACCACCG  ACGTAACCGG  CGCGGTTACT  TTGGAAGAAG  GCGTGGAAAT        750
    5    GGTAATGCCC  GGTGAGAACG  TAACCATTAC  TGTAGAACTG  ATTGCGCCTA        800
         TCGCTATGGA  AGAAGG                                               816
```

```
    10   2) INFORMATION FOR SEQ ID NO: 128

            (i) SEQUENCE CHARACTERISTICS:
                 (A)    LENGTH: 831 bases
                 (B)    TYPE: Nucleic acid
    15           (C)    STRANDEDNESS: Double
                 (D)    TOPOLOGY: Linear

           (ii) MOLECULE TYPE: Genomic DNA

    20     (vi) ORIGINAL SOURCE:
                 (A)    ORGANISM: Neisseria meningitidis
                 (B)    STRAIN: ATCC 13077

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128
    25
         CGGTGCAATC  CTGGTATGTT  CCGCAGCCGA  CGGTCCTATG  CCGCAAACCC         50
         GCGAACACAT  CCTGCTGGCC  CGTCAAGTAG  GCGTACCTTA  CATCATCGTG        100
         TTCATGAACA  AATGCGACAT  GGTCGACGAT  GCCGAGCTGT  TGGAACTGGT        150
         TGAAATGGAA  ATCCGCGACC  TGCTGTCCAG  CTACGACTTC  CCCGGCGACG        200
    30   ACTGCCCGAT  CGTACAAGGT  TCCGCACTGA  AAGCCTTGGA  AGGCGATGCC        250
         GCTTACGAAG  AAAAAATCTT  CGAATTGGCT  GCTGCATTGG  ACAGCTACAT        300
         CCCGACTCCC  GAGCGTGCCG  TGGACAAACC  TTTCTTGTTG  CCTATCGAAG        350
         ACGTATTCTC  TATTTCCGGT  CGTGGTACAG  TAGTAACCGG  TCGTGTAGAG        400
         CGCGGTATCA  TCCACGTCGG  TGACGAGATC  GAAATCGTCG  GTCTGAAAGA        450
    35   AACTCAAAAA  ACCACTTGTA  CCGGTGTTGA  AATGTTCCGC  AAACTGCTGG        500
         ACGAAGGTCA  AGCAGGCGAC  AACGTAGGCG  TATTGCTGCG  CGGTACCAAA        550
         CGTGAAGACG  TAGAGCGTGG  TCAAGTATTG  GCTAAACCGG  GTACAATCAC        600
         TCCTCACACC  AAGTTCAAAG  CAGAAGTATA  CGTACTGAGC  AAAGAAGAGG        650
         GCGGCCGCCA  TACCCCGTTC  TTCGCCAACT  ACCGTCCCCA  ATTCTACTTC        700
    40   CGTACCACCG  ACGTAACCGG  CGCGGTTACT  TTGGAAGAAG  GTGTGGAAAT        750
         GGTAATGCCG  GGCGAGAACG  TAACCATCAC  CGTAGAACTG  ATTGCGCCTA        800
         TCGCTATGGA  AGAAGGTTTG  CGCTTTGCGA  T                            831
```

```
    45
         2) INFORMATION FOR SEQ ID NO: 129

            (i) SEQUENCE CHARACTERISTICS:
                 (A)    LENGTH: 815 bases
    50           (B)    TYPE: Nucleic acid
                 (C)    STRANDEDNESS: Double
                 (D)    TOPOLOGY: Linear

           (ii) MOLECULE TYPE: Genomic DNA

    55
           (vi) ORIGINAL SOURCE:
                 (A)    ORGANISM: Neisseria mucosa
                 (B)    STRAIN: ATCC 19696

    60     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129
```

78

```
        CGGCGCAATC TTGGTATGTT CTGCTGCYGA CGGTCCTATG CCGCAAACCC        50
        GYGAACACAT CCTGTTGGCC CGTCAAGTAG GYGTACCTTA CATCATCGTG       100
        TTCATGAACA AATGCGACAT GGTTGACGAT GCCGAAYTGT TGGAACTGGT       150
    5   TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCTGGYGACG       200
        ACTGCCCGAT TGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGATGCC       250
        GCTTACGAAG AAAAAATCTT CGAACTGGCT GCCGCATTGG ACAGCTACAT       300
        CCCGACTCCC GAGCGTGCCG TAGACAAACC GTTCCTGTTG CCTATCGAAG       350
        ACGTATTCTC CATCTCCGGT CGTGGTACAG TAGTAACCGG CCGTGTAGAG       400
   10   CGCGGTGTTA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA       450
        AACCCAAAAA ACCACATGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG       500
        ACGAAGGTCA AGCCGGTGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA       550
        CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC       600
        TCCGCACACC AAATTCAAAG CAGAAGTGTA CGTATTGAGC AAAGAAGAGG       650
   15   GTGGTCGTCA TACTCCGTTC TTCGCTAACT ACCGTCCTCA ATTCTACTTC       700
        CGTACTACCG ACGTAACCGG TGCGGTTACT TTGGAAGAAG GTGTAGAAAT       750
        GGTTATGCCT GGTGAGAAYG TAGCCATYAC TGTAGAACTG ATTGCGCCTA       800
        TYGCTATGGA AGAAG                                            815
```

20

2) INFORMATION FOR SEQ ID NO: 130

```
        (i) SEQUENCE CHARACTERISTICS:
   25       (A)     LENGTH: 829 bases
            (B)     TYPE: Nucleic acid
            (C)     STRANDEDNESS: Double
            (D)     TOPOLOGY: Linear

   30   (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
            (A)     ORGANISM: Neisseria sicca
            (B)     STRAIN: ATCC 9913
   35
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130
```

```
        GGCGCAATCT TGGTATGTTC CGCTGCTGAC GGTCCTATGC CGCAAACCCG        50
        CGAACACATC CTGTTGGCCC GCCAAGTAGG CGTACCTTAC ATCATCGTGT       100
   40   TCATGAACAA ATGCGACATG GTTGACGATG CCGAGCTGTT GGAACTGGTT       150
        GAAATGGAAA TCCGTGACTT GCTGTCAAGC TACGACTTCC CTGGTGACGA       200
        CTGCCCGATC GTACAAGGTT CTGCACTGAA AGCCTTGGAA GGCGACGCCG       250
        CTTACGAAGA AAAAATCTTC GAACTGGCTG CTGCATTGGA CAGCTACATC       300
        CCGACTCCTG AGCGTGCCGT GGACAAACCG TTCCTGTTGC CTATTGAAGA       350
   45   CGTATTCTCC ATCTCCGGTC GCGGTACCGT AGTAACCGGC CGTGTAGAGC       400
        GCGGTGTTAT CCACGTTGGT GACGAGATTG AAATCGTAGG TCTGAAAGAA       450
        ACCCAAAAAA CCACTTGTAC CGGTGTTGAA ATGTTCCGCA AACTGCTGGA       500
        CGAAGGTCAA GCCGGTGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC       550
        GTGAAGAAGT GGAACGCGGT CAAGTATTGG CTAAACCGGG TACCATCACT       600
   50   CCTCACACTA AATTCAAAGC AGAAGTTTAC GTATTGAGTA AAGAAGAGGG       650
        TGGTCGTCAT ACTCCGTTCT TCGCTAACTA CCGTCCTCAA TTCTACTTCC       700
        GTACTACCGA CGTAACCGGC GCGGTTACTT TGGAAGAAGG TGTAGAAATG       750
        GTTATGCCTG GTGAGAACGT AGCCATCACT GTAGAACTGA TTGCACCGAT       800
        CGCTATGGAA GAAGGTCTGC GCTTTGCGA                             829
```

55

2) INFORMATION FOR SEQ ID NO: 131

60   (i) SEQUENCE CHARACTERISTICS:

79

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5

        (A)   LENGTH: 814 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

   (ii)MOLECULE TYPE: Genomic DNA

   (vi)ORIGINAL SOURCE:
        (A)   ORGANISM: *Neisseria subflava*
10   (B)   STRAIN: ATCC 14221

   (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 131

```
     CGGCGCGACT TGGTATGTTC CGCAGCTGAT GGTCCTATGC CTCAAACTCG     50
15   CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT    100
     TCATGAACAA ATGCGACATG GTTGACGATG CCGAGCTGTT GGAACTGGTT    150
     GAAATGGAAA TCCGTGACCT GTTGTCAAGC TACGACTTCC CAGGCGACGA    200
     CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGACGCTG    250
     GTTACGAAGA GAAAATCTTC GAATTGGCTG CTGCTCTGGA CAGCTACATC    300
20   CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA    350
     CGTATTCTCT ATCTCTGGCC GTGGTACAGT AGTAACTGGT CGTGTAGAGC    400
     GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA    450
     ACCCAAAAAA CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA    500
     CGAAGGTCAA GCTGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACCAAAC    550
25   GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATTACT    600
     CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG    650
     TGGTCGTCAC ACTCCATTCT TCGCTAACTA CCGTCCACAA TTCTACTTCC    700
     GTACTACTGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG    750
     GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT    800
30   CGCTATGGAA GAAG                                          814
```

   2)INFORMATION FOR SEQ ID NO: 132
35
        (i)SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 818 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
40   (D)   TOPOLOGY: Linear

   (ii)MOLECULE TYPE: Genomic DNA

   (vi)ORIGINAL SOURCE:
45   (A)   ORGANISM: *Neisseria weaveri*
        (B)   STRAIN: ATCC 51223

   (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 132

```
50   GCCATCTTGG TATGTTCTGC TGCTGACGGT CCTATGCCGC AAACCCGTGA     50
     GCACATCCTG TTGGCTCGTC AAGTAGGTGT ACCCTACATC ATCGTATTCA    100
     TGAACAAATG CGATATGGTT GATGATGCAG AGCTGCTGGA ATTGGTAGAA    150
     ATGGAAATCC GTGATCTGCT GAGCAGCTAC GATTTCCCTG GCGATGATTG    200
     YCCAATCGTG CAAGGTTCTG CTTTGAAAGC TTTGGAAGGT GATGCCGCTT    250
55   ACGAAGAAAA AATCTTTGAA TTAGCTGCTG CATTGGATAG CTATATTCCA    300
     ACWCCTGAGC GYGCTGTTGA TAAACCATTC CTGTTGCCGA TTGAAGATGT    350
     ATTCTCAATT TCAGGTCGTG GTACAGTAGT AACTGGTCGT GTAGAGCGCG    400
     GTATTATTCA CGTAGGCGAT GAAATTGAAA TTGTAGGTTT GAAAGARACY    450
     CAAAAAACTA CTTGTACCGG CGTTGAAATG TTCCGTAAAT GCTGGATSA     500
60   AGGTCAGGCT GGTGATAACG TAGGCGTATT GTTGCGTGGT ACCAAACGTG    550
```

```
     AAGACGTTGA  GCGTGGTCAA  GTATTGGCTA  AGCCTGGTWC  TATTACTCCG        600
     CAYACCAAAT  TCAAAGCAGA  RGTKTATGTW  TTGAGYAAGG  AAGAAGGCGG        650
     TCGTCATACT  CCGTTCTTCG  CTAACTATCG  TCCGCAATTC  TATTTCCGTA        700
     CTACAGACGT  TACCGGTGCK  GTRACTTTAG  AAGAAGGTGT  GGAAATGGTA        750
   5 ATGCCTGGTG  AGAAYGTTGC  CATTACTGTW  GARYTGATYG  CTCCGATTGC        800
     KATGGAAGAA  GGYTGCGT                                             818
```

10   2) INFORMATION FOR SEQ ID NO: 133

        (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 836 bases
            (B)   TYPE: Nucleic acid
15   (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

20   (vi) ORIGINAL SOURCE:
            (A)   ORGANISM: *Ochrobactrum anthropi*
            (B)   STRAIN: ATCC 49188

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25
```
     CGGCGCAATT  CTGGTTGTTT  CGGCCGCTGA  CGGCCCGATG  CCGCAGACCC         50
     GTGAGCACAT  CCTGCTCGCT  CGTCAGGTTG  GCGTTCCGGC  AATCGTCGTG        100
     TTCCTGAACA  AGTGCGACCA  GGTTGACGAT  GCAGAACTGC  TCGAACTGGT        150
     TGAACTGGAA  GTTCGCGAAC  TTCTGTCGAA  ATACGATTTC  CCGGGCGACG        200
  30 AAGTTCCGAT  CATCAAGGGC  TCGGCTCTTG  CTGCTCTGGA  AGATTCTTCG        250
     AAGGAACTGG  GCGAAGACGC  CGTTCGTTCG  CTGATGGCCG  CTGTTGACGA        300
     CTACATTCCG  ACCCCGGAAC  GTCCGATCGA  CCAGCCGTTC  CTGATGCCGA        350
     TCGAAGACGT  TTTCTCGATC  TCGGGCCGTG  GTACGGTTGT  GACGGGTCGC        400
     GTTGAGCGCG  GTATCGTCAA  GGTTGGTGAA  GAAGTTGAAA  TCGTCGGCAT        450
  35 CAAGGCGACG  GCGAAGACGA  CGGTAACCGG  CGTTGAAATG  TTCCGCAAGC        500
     TGCTCGAYCA  GGGCCAGGCT  GGCGACAACA  TCGGCGCTCT  GATCCGCGGC        550
     GTTGGCCGTG  AAGACGTTGA  ACGCGGCCAG  GTTCTCTGCA  AGCCGGGTTC        600
     TGTGAAGCCG  CACACCAAGT  TCAAGGCAGA  AGCCTACATT  CTGACCAAGG        650
     ACGAAGGTGG  CCGTCATACG  CCGTTCTTTA  CGAACTACCG  TCCGCAGTTC        700
  40 TACTTCCGCA  CGACGGACGT  GACCGGTGTT  GTCACGCTGC  CGGAAGGCAC        750
     GGAAATGGTT  ATGCCTGGCG  ACAACGTCGC  TATGGACGTC  ACCCTGATCG        800
     TGCCGATCGC  CATGGAAGAG  AAGCTCCGCT  TCGCTA                        836
```

45
     2) INFORMATION FOR SEQ ID NO: 134

        (i) SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 805 bases
50   (B)   TYPE: Nucleic acid
            (C)   STRANDEDNESS: Double
            (D)   TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

55   (vi) ORIGINAL SOURCE:
            (A)   ORGANISM: *Pantoea agglomerans*
            (B)   STRAIN: ATCC 27155

60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

81

```
        CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA        50
        TCCTGCTGGG TCGTCAGGTT GGCGTTCCTT ACATCATCGT GTTCCTGAAC        100
        AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAACTGG TAGAGATGGA        150
     5  AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA        200
        TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA        250
        GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCCGGATCC        300
        AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT        350
        CAATCTCTGG CCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGCATC        400
     10 GTTAAAGTCG GCGACGAAGT TGAAATCGTG GGTATCAAAG ATACTGCGAA        450
        ATCAACCTGT ACCGGTGTTG AGATGTTCCG TAAGCTGCTG GACCAGGGTC        500
        AGGCAGGCGA AAACTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC        550
        ATCCAGCGTG GCCAGGTTCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC        600
        CCAGTTCGAG TCAGAAGTTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC        650
     15 ATACTCCGTT CTTCAAAGGC TATCGTCCAC AGTTCTACTT CCGTACAACT        700
        GATGTAACCG GTTCAGTAGA GCTGCCAGAA GGCGTTGAGA TGGTCATGCC        750
        AGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG        800
        ACGAA                                                        805
```

     20

     2) INFORMATION FOR SEQ ID NO: 135

        (i) SEQUENCE CHARACTERISTICS:
     25   (A)   LENGTH: 825 bases
             (B)   TYPE: Nucleic acid
             (C)   STRANDEDNESS: Double
             (D)   TOPOLOGY: Linear

     30 (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
             (A)   ORGANISM: *Pantoea dispersa*
             (B)   STRAIN: ATCC 14589
     35
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

```
        CGCGATCCTG GTTGTTGCTG CGACTGATGG CCCAATGCCT CAGACCCGTG        50
        AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC        100
     40 CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA        150
        GATGGAAGTT CGCGATCTGC TGTCTCAGTA CGACTTCCCA GGCGACGATA        200
        CCCCAATCGT ACGCGGTTCT GCGCTGAAAG CGCTGGAAGG CGACGCTGAG        250
        TGGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC        300
        AGATCCAGTA CGTGCTATCG ATCTGCCGTT CCTGCTGCCA ATCGAAGACG        350
     45 TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCG TGTTGAGCGC        400
        GGCATCGTGA AAGTGGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC        450
        TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAAA CTGCTGGACC        500
        AGGGTCAGGC AGGCGAGAAC TGTGGTGTTC TGCTGCGCGG TATCAAGCGT        550
        GAAGAGATCC AGCGTGGTCA GGTTCTGGCT AAGCCAGGCA CCATCAAGCC        600
     50 ACACACCAAG TTCGTATCAG AAGTGTACGT ACTGTCTAAA GACGAAGGCG        650
        GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT        700
        ACYACTGATG TGACCGGCAM CATMGAACTG CCAGAAGGCG TTGAGATGGT        750
        AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG        800
        CGATGGACCA GGGTCTGCGT TTCGC                                   825
```

     55

     2) INFORMATION FOR SEQ ID NO: 136

     60 (i) SEQUENCE CHARACTERISTICS:
                                    82

       (A)   LENGTH: 762 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

  (ii)MOLECULE TYPE: Genomic DNA

  (vi)ORIGINAL SOURCE:
       (A)   ORGANISM: *Pasteurella multocida*
       (B)   STRAIN: NCTC 10322

  (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 136

```
CACAAACACG TGAGCACATC CTTTTAGGTC GCCAAGTAGG CGTTCCTTAC    50
ATCATCGTAT TCTTAAACAA ATGCGACATG GTGGATGATG AAGAATTATT   100
AGAATTAGTT GAAATGGAAG TGCGTGAACT TCTTTCTCAA TATGATTTCC   150
CAGGTGATGA TACACCAATC GTACGTGGTT CAGCGTTACA AGCGTTAAAC   200
GGYGTAGCTG AGTGGGAAGA GAAAATTCTT GAGTTAGCCA ACCACTTAGA   250
TACTTACATT CCAGAGCCAC AACGTGCAAT CGACCAACCG TTCCTTCTTC   300
CGATTGAAGA CGTGTTCTCA ATTTCTGGTC GTGGTACAGT AGTAACAGGT   350
CGTGTTGAGC GTGGTATCAT CCGTACAGGT GAAGAGGTTG AAATTGTTGG   400
TATTAAAGCG ACAACGAAGA CCACAGTAAC AGGTGTTGAG ATGTTCCGTA   450
AATTATTAGA CGAAGGTCGT GCGGGTGAGA ACGTTGGTGC TTTATTACGT   500
GGTACTAARC GTGAAGAAAT CGAACGTGGT CAAGTGTTAG CGAAACCGGG   550
TTCAATYACG CCACACACTG ATTTTGAATC AGAAGTTTAC GTGTTATCAA   600
AAGAAGAAGG TGGTCGTCAT ACACCATTCT TCAAAGGTTA CCGTCCACAG   650
TTCTACTTCC GTACAACGGA CGTAACAGGT ACAATCGAAT TACCGGAAGG   700
TGTTGAGATG GTGATGCCTG GTGATAACAT CAAGATGACT GTAAGTTTGA   750
TTCACCCAAT CG                                            762
```

2)INFORMATION FOR SEQ ID NO: 137

  (i)SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 832 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

  (ii)MOLECULE TYPE: Genomic DNA

  (vi)ORIGINAL SOURCE:
       (A)   ORGANISM: *Peptostreptococcus anaerobius*
       (B)   STRAIN: ATCC 27337

  (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 137

```
TGGAGCTATC TTAGTTGTAT CAGCAGCGGA TGGACCAATG CCACAAACAA    50
GAGAACACAT CTTATTATCA AGACAAGTAG GAGTACCATA TATCGTAGTA   100
TATTTGAATA AAGCAGATAT GGTAGAAGAT GAAGAATTAT TAGAATTAGT   150
AGAAATGGAA GTAAGAGAAT TACTATCTGA ATATGGATTC CCAGGAGATG   200
AAATTCCAAT CATAACAGGA TCATCCTTAG GAGCATTAAA TGGAGAACAA   250
AAATGGATAG ATCAAATCAT GGCATTGATG AAAGCCGTAG ATGAATATAT   300
TCCAACACCG GAAAGAGCAG TAGATCAACC ATTCTTGATG CCAATCGAAG   350
ACGTATTTAC AATTACAGGA AGAGGAACTG TAGTAACAGG AAGAGTTGAA   400
AGAGGAGTTG TAAAAGTWGG AGAAGAAGTT GAAATCGTAG GAATCAAAGC   450
GACAACAAAG ACAACTTGTA CYGGAGTAGA AATGTTCCGA AAATTATTGG   500
ATCAAGGACA AGCAGGAGAT AACATCGGAG CTTTATTRAG AGGAACCAAG   550
AAAGAAGATG TAGAAAGAGG ACAAGTATTG GCAAAACCAG GAACAATTCA   600
```

```
     TCCTCATACA AACTTCAGTG GAGAAGTATA TGTATTGACA AAAGAAGAAG    650
     GAGGAAGACA TACTCCATTC TTCTCAGGAT ACAGACCACA ATTTTACTTT    700
     AGAACCACAG ATATTACAGG AGCAGTAACA TTACCAGAAG GAGTAGAAAT    750
     GGTAATGCCR GGAGATAATA TCACAATGAC AGTAGAATTG ATTCACCCAA    800
   5 TTGCAATGGA AACAGGATTA CGATTTGCAA TT                       832
```

2) INFORMATION FOR SEQ ID NO: 138

10
     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 823 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
15   (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
20   (A)   ORGANISM: *Peptostreptococcus asaccharolyticus*
        (B)   STRAIN: LSPQ 2639

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

```
25 TAGTATGTTC AGCAGCAGAY GGTCCAATGC CACAAACAAG AGAACACATT     50
     CTACTAGCAA GACAAGTTGG TGTACCAAAG ATAGTAGTAT TCCTAAACAA    100
     AGAAGACCAA GTAGACGATC CAGAACTAAT TGAATTAGTA GAGATGGAAA    150
     TCAGAGACCT ACTATCAGAA TATGACTTCG AYGGAGACAA CACACCAATC    200
     GTAGTAGGAT CAGCATTAAA AGCCCTAGAC GATCCAGACG GAGAATGGGG    250
30 AGACAAAATC GTAAAACTAA TGGAAGMAGT AGACGAATAC ATCCCAACAC    300
     CAGTAAGAGA TACAGAACAC CCATTCCTAA TGCCAATCGA AGACRTATTC    350
     TCAATYACAG GAAGAGGAAC AGTAGCAACA GGAAGAGTAG AACAAGGTGT    400
     AGTAAAAGTA GGMGACACAG TAGAACTAGT AGGCTTAACA GACGAAAGCA    450
     GACAAGTAGT AGTAACAGGT GTAGAAATGT TTAGAAAACA ACTAGACCTA    500
35 GCAGAAGCMG GAGACAACAT TGGAGCCCTA CTAAGAGGAG TACAAAGAGA    550
     AGAAATCCAA AGAGGACAAG TACTAGCAGC ACCAGGAACA ATCAAACCAC    600
     ACACAAAATT TGAAGCAGAA GTATACGTAC TAACAAAAGA AGAAGGTGGA    650
     AGACACACAC CATTCTTTAA CGGATACAGA CCACAATTCT ACTTCAGAAC    700
     AACAGACGTA ACAGGAGACA TCCAACTAGC AGACGGAGTA GAAATGGTAA    750
40 TGCCAGGAGA CAACTCAACA TTTACAGTAA CACTAATCAC ACCAATCGCA    800
     ATGGACGAAG GACTAAGATT CGC                                 823
```

45   2) INFORMATION FOR SEQ ID NO: 139

     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 832 bases
        (B)   TYPE: Nucleic acid
50   (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

55   (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Peptostreptococcus prevotii*
        (B)   STRAIN: ATCC 9321

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60

```
          CTATCATCGT AGTATCTGCA GCAGACGGTC CAATGCCCAA ACAGAGAGAA        50
          CACATCCTAC TAGCAAGACA AGTAGGCGTT CCAAAAATCG CAGTATTCCT       100
          AAACAAAGAA GACCAAGTAG ACGATCCAGA ACTAATCGAA TTAGTAGAAA       150
          TGGAAATCAG AGACCTACTT TCAGAATACG ACTTCGATGG AGACAACGCT       200
5         CCAGTAGTAG TAGGATCTGC TCTTAAATCA CTAGAAGAAG GCGGAGAAGG       250
          CCCATGGTCA GACAAAATCC TTGACCTAAT GGCACAAGTA GACGAATACT       300
          TCGACATCCC AGAAAGAGAC AACGACCAAC CATTCCTAAT GCCAGTAGAA       350
          GACGTAATGA CAATCTCAGG ACGTGGAACA GTAGCAACAG GAAGAGTTGA       400
          AAGAGGAACA CTAAAAGTTG GTGATACAGT AGAAATCGTA GGACTAACAG       450
10        AAGATACAAA AGAAACAGTA GTAACTGGAG TAGAAATGTT CCACAAATCM       500
          CTAGACCAAG CAGAATCTGG AGATAACGTA GGACTACTAC TAAGAGGAGT       550
          AACAAGAGAT CAAATCTCAA GAGGACAAGT ACTAGCAAAA CCAGGWTCAG       600
          TAAACCCACA CACAGAATTC GAAGGTCAAG TATACGTACT AACAAAAGAA       650
          GAAGGTGGAC GTCACACACC ATTCTTCAGT GGATATAGAC CACAATTCTT       700
15        CTTTAGAACA ACAGACGTAA CAGGAGACAT CGAACTAGAA GAAGGCGTAG       750
          AAATGGTAAT GCCAGGAGAC AACGCAACAT TCAAAATCAC ACTCCAAAAA       800
          CCAATCGCTC TAGAAGAAGG ACTAAGATTC GC                         832
```

20   2) INFORMATION FOR SEQ ID NO: 140

          (i) SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 831 bases
25   (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

          (ii) MOLECULE TYPE: Genomic DNA
30
          (vi) ORIGINAL SOURCE:
                (A)   ORGANISM: *Porphyromonas asaccharolytica*
                (B)   STRAIN: ATCC 25260

35   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

```
          CGGTGCTATC ATCGTAGTTG CTGCAACTGA TGGTCCTATG CCTCAGACGC        50
          GTGAGCACAT CCTACTAGCA CGTCAGGTCA ACGTACCTCG TCTAGTTGTC       100
          TTTATGAACA AGTGCGACCT TGTTGATGAC GAGGAGATGC TCGAGCTCGT       150
40        AGAGATGGAT ATGCGTGAGC TACTAAGCTT CTATGACTTT GACGGCGACA       200
          ACACTCCTGT CATCCGTGGT TCTGCTCTTG GTGCTCTCAA TGGTGAGCCT       250
          AAGTGGGTAG AGAAGGTTAT GGAGCTCATG GAGGCTGTAG ACACTTGGAT       300
          CCCACTACCT GAGCGCGACA TCGACAAGCC TTTCCTAATG CCTGTAGAGG       350
          ACGTATTCTC TATCACAGGT CGTGGTACTG TCGCTACTGG TCGTATCGAG       400
45        ACTGGTGTCG TTAAGGTCAA CGATGAGGTT CAGATCATCG GTCTAGGTGC       450
          TGAGGGTAAG AAGAGCGTCG TAACTGGCGT GGAAATGTTC CGCAAGATCC       500
          TTGATGAGGG TGAAGCTGGT GATAACGTAG GTCTCCTACT CCGTGGTATC       550
          GACAAGGACG AGATCAAGCG CGGTATGGTC CTAGCACACC CAGGTCAGGT       600
          CAAGCCTCAC GATCACTTCA AGGCTGAGGT CTATATCCTG AAGAAGGAAG       650
50        AGGGTGGTCG TCACACACCA TTCCACAACA AGTACCGTCC TCAGTTCTAC       700
          ATCCGTACGC TAGACGTAAC GGGCGAGATC ACACTCCCAG AGGGTGTAGA       750
          GATGGTTATG CCTGGTGATA ACGTCACCAT CGATGTCAAG CTCATCTCTC       800
          CAGTAGCTTG TAGCGTAGGT CTACGCTTCG C                         831
```

55

        2) INFORMATION FOR SEQ ID NO: 141

          (i) SEQUENCE CHARACTERISTICS:
60   (A)   LENGTH: 818 bases

                                        85

SUBSTITUTE SHEET (RULE 26)

```
          (B)   TYPE: Nucleic acid
          (C)   STRANDEDNESS: Double
          (D)   TOPOLOGY: Linear

5      (ii)MOLECULE TYPE: Genomic DNA

       (vi)ORIGINAL SOURCE:
          (A)   ORGANISM: Porphyromonas gingivalis
          (B)   STRAIN: ATCC 33277

10     (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 141
```

```
        CGGTGCTATA ATCGTTGTAG CAGCTACAGA CGGTCCTATG CCTCAGACTC      50
        GCGAGCACAT CCTTTTGGCT CGCCAGGTAA ACGTTCCTCG TCTGGTTGTT     100
15      TTCATGAACA AATGTGACAT GGTAGACGAT GAAGAGATGC TCGAGCTTGT     150
        TGAAATGGAC ATGCGCGAAC TCCTTTCTTT CTACGATTTC GATGGTGACA     200
        ATACCCCTAT CATCCGTGGT TCTGCTCTGG GCGCTTTGAA TGGAGAGCCT     250
        CAGTGGGAAG ACAAGGTGAT GGAGCTTATG GAAGCTGTTG ACAACTGGGT     300
        TCCCCTGCCT GAGCGCGATA TCGACAAACC GTTCTTGATG CCGGTTGAAG     350
20      ACGTGTTCTC TATCACGGGT CGTGGTACGG TCGCTACAGG ACGTATCGAA     400
        ACCGGTATTG TGAAGACCGG TGACGAAGTT CAAATCATCG GCCTCGGTGC     450
        AGAAGGAATG AAGTCGGTTG TTACGGGTGT TGAAATGTTC CGTAAGATTC     500
        TTGACGAAGG TCAGGCTGGT GACAACGTTG GTCTCCTCCT GCGTGGTATC     550
        GATAAGGATC AGATCAAGCG TGGTATGGTT ATCTCTCACC CGGGTAAGAT     600
25      TACTCCTCAC AAGAGATTTA AGGCCGAGGT TTATATCTTG AAGAAAGAAG     650
        AAGGTGGTCG CCACACTCCT TTCCACAACA AATATCGTCC GCAGTTCTAC     700
        ATCCGTACGC TTGACGTGAC CGGTGAAATC ACTCTTCCCG AAGGAACAGA     750
        AATGGTTATG CCCGGTGACA ACGTAACGAT CACTGTAGAA CTCATCTACC     800
        CGGTTGCATG TAATGTAG                                        818
30
```

```
    2)INFORMATION FOR SEQ ID NO: 142

35     (i)SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 830 bases
          (B)   TYPE: Nucleic acid
          (C)   STRANDEDNESS: Double
          (D)   TOPOLOGY: Linear
40
       (ii)MOLECULE TYPE: Genomic DNA

       (vi)ORIGINAL SOURCE:
          (A)   ORGANISM: Pragia fontium
45        (B)   STRAIN: ATCC 49100

       (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 142
```

```
        CGGCGCTATT CTGGTTGTTG CTGCAACTGA TGGTCCTATG CCTCAAACTC      50
50      GTGAGCACAT CCTGTTAGGY CGCCAGGTTG GCGTACCATA CATCATTGTG     100
        TTCCTGAACA AGTGTGACAT GGTTGAYGAT GAAGAGCTGT TAGAACTGGT     150
        TGAAATGGAA GTTCGTGAGC TTCTGTCTCA GTACGATTTC CCAGGTGATG     200
        ATACTCCAGT TGTTCGTGGT TCTGCGCTGA AAGCGTTRGA AGGCGAAGCT     250
        GAGTGGGAAG CTAAAATCAT TGAATTGGCT GACTCCCTGG AYAGCTACAT     300
55      TCCACAGCCA GAGCGTGCAA TTGATAAGCC GTTCCTGCTG CCAATCGAAG     350
        ACGTTTTCTC AATCTCTGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG     400
        CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
        TACTGTGAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AARTTACTGG     500
        ATGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAG     550
60      CGTGATGAAA TCGAACGTGG TCAAGTATTA GCAAAACCAG GTTCAATCAA     600
```

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```
     CCCGCATACT AACTTCGTAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG      650
     GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTYTACTTC      700
     CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT      750
     GGTAATGCCA GGTGATAACA TTCAGATGAC TGTAACTCTG ATTGCCCCAA      800
   5 TCGCGATGGA CGAAGGTTTA CGCTTCGCTA                            830
```

2) INFORMATION FOR SEQ ID NO: 143

     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 821 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Prevotella melaninogenica*
        (B)   STRAIN: ATCC 25845

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

```
     TGGTGCTATC TTGGTTGTAG CTGCTACTGA TGGTCCTATG CCTCAGACTC      50
     GTGAGCACGT ATTGCTCGCT CGTCAGGTAA ACGTACCTCG CTTGGTTGTA      100
     TTCTTGAACA AGTGTGATAT GGTTGACGAT GCTGAGATGC TTGACCTCGT      150
     TGAGATGGAG GTTCGTGAGA TCCTCGAGCA GTACGGTTAT GAGGAGGATA      200
     CTCCTATTAT TCGTGGTTCT GCACTCGGTG CTTTGAACGG TGTTGAGAAG      250
     TGGGTAGACT CTGTAATGGA GCTCATGGAT ACTGTTGACA CTTGGATTGA      300
     AGAGCCAGAG CGTGAGATTG ACAAGCCATT CTTGATGCCT GTTGAGGACG      350
     TATTCTCTAT CACAGGTCGT GGTACTGTAG CTACTGGTCG TATCGAGACT      400
     GGTATCTGTA AGGTAGGTGA TGAGGTTCAG TTGCTCGGTC TCGGTGAGGA      450
     CAAGAAGTCT GTTATCACTG GTGTTGAGAT GTTCCGTAAG AACCTTCCAA      500
     CAGGTCAGGC TGGTGACAAC GTAGGTCTCC TCCTTCGTGG TATCGATAAG      550
     GCTGAGGTTA AGCGTGGTAT GGTTGTTGTG CACCCAGGTG CTATTACTCC      600
     TCACGATCAC TTCAAGGCAT CTATCTATGT ATTGAAGAAG GAAGAGGGTG      650
     GTCGTCATAC TCCATTCGGT AACAAGTATC GTCCACAGTT CTACCTCCGT      700
     ACAATGGACT GTACAGGTGA AATCCACCTC CCAGAGGGCG TTGAGATGGT      750
     TATGCCAGGT GACAACGTAG AGATTGAAGT TGTATTGATC TATAAGGTTG      800
     CTTTGAACGA GGGTCTTCGT T                                     821
```

2) INFORMATION FOR SEQ ID NO: 144

     (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 827 bases
        (B)   TYPE: Nucleic acid
        (C)   STRANDEDNESS: Double
        (D)   TOPOLOGY: Linear

     (ii) MOLECULE TYPE: Genomic DNA

     (vi) ORIGINAL SOURCE:
        (A)   ORGANISM: *Prevotella oralis*
        (B)   STRAIN: ATCC 33269

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

87

```
        TGGTGCTATT CTTGTAGTAG CTGCTACTGA CGGTCCTATG CCTCAAACTC          50
        GTGAACACGT GCTTCTTGCT CGTCAGGTGA ACGTACCTCG TTTGGTCGTT         100
        TTCTTGAACA AGTGCGATAT GGTTGACGAT GAAGAAATGC TTGAGCTCGT ·       150
        AGAAATGGAG CTTCATGAAC TTCTCGAGCA GTATGAATAT GAGGAGGATA         200
    5   CTCCTATTGT TCGTGGTTCG GCACTTGGCG CTCTGAATGG AGTAGAGAAG         250
        TGGGTTGACA GCGTGATGAA GTTGATGGAT ACCGTTGATG AATGGATACA         300
        GGAACCACCG CGTGATCTTG ATAAGCCTTT CTTGATGCCG GTAGAGGATG         350
        TATTTTCTAT TACTGGTCGT GGAACGGTTG TTACAGGCCG TATTGAAACT         400
        GGTAAGGTTA AGGTGGGCGA TGAAGTTCAA CTTCTTGGTC TCGGTGAAGA         450
   10   TAAGAAGTCC GTTGTGACAG GCGTTGAGAT GTTCCGTAAG ATTCTTGACG         500
        AAGGTGAAGC TGGTGATAAT GTAGGCTTGC TGCTTCGTGG TATCGATAAG         550
        ACGGAAGTAA AGCGTGGTAT GGTTGTCGTA CATCCGGGGG CTATTACTCC         600
        TCACGATCAT TTCAAGGCTT CAGTTTACGT ATTGAAGAAA GAAGAAGGCG         650
        GTCGCCATAC TCCGTTTGGT AMCAAGTATC GTCCACAGTT CTATCTTCGT         700
   15   ACCATGGACT GTACTGGTGA AATTACTCTT CCGGAAGGAG TTGAGATGGT         750
        AATGCCGGGT GATAACGTCG AAATTGAAGT TAAGTTGATC TATCCGGTAG         800
        CTTTGAACGA GGGACTTCGT TTCGCTA                                  827
```

   20
        2) INFORMATION FOR SEQ ID NO: 145

            (i) SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 833 bases
   25   (B)   TYPE: Nucleic acid
                (C)   STRANDEDNESS: Double
                (D)   TOPOLOGY: Linear

            (ii) MOLECULE TYPE: Genomic DNA
   30
            (vi) ORIGINAL SOURCE:
                (A)   ORGANISM: *Propionibacterium acnes*
                (B)   STRAIN: ATCC 6919

   35   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

```
        CGGCGCCATC CTCGTGGTTG CTGCTACCGA CGGCCCGATG CCTCAGACTC          50
        GCGAGCACGT TCTGCTCGCT CGTCAGGTGG GCGTGCCCGC CATCGTCGTC         100
        GCCCTCAACA AGTGCGACAT GGTTGACGAT GAGGAGCTCA TTGAGCTCGT         150
   40   CGAGATGGAG GTCCGCGAGC TGCTGACCTC GCAGGAGTTC GACGGCGACA         200
        ACTGCCCTGT CGTTCGCATC TCCGCCTTCC AGGCCCTCCA GGGTGATGAG         250
        AAGTGGACCC AGTCGATCCT CGACCTCATG GACGGCCGTGG ACGAGTACAT         300
        CCCGCAGCCT GAGCGCGATC TCGACAAGCC CTTCCTTATG CCGATCGAGG         350
        ACGTCTTCAC CATCACCGGC CGTGGCACCG TTGTCACCGG TCGTGTCGAG         400
   45   CGCGGCGTCG TCAAGACTGG CGAAGAGGTC GAGATCGTCG GTATCCACGA         450
        GAAGACCCAG AAGACCACCG TTACCGGTGT CGAGATGTTC CGCAAGATCC         500
        TCGACGAGGG CCGCGCTGGT GAGAACGTCG GCGTTCTGCT CCGTGGCACC         550
        AAGAAGGAGG ATGTCGTTCG CGGCATGGTC CTCTCCAAGC CTGGTTCCAC         600
        CACCCCCCAC ACCGACTTCG AGGGCCAGGT CTACGTCCTC AAGAAGGATG         650
   50   AGGGTGGCCG CCACAAGCCG TTCTTCTCCC ACTACAGCCC CCAGTTCTAC         700
        TTCCGTACCA CGGACGTGAC TGGCACTGTT GAGCTCCCCG AGGGCACCGA         750
        GATGGTCATG CCTGGCGACA ACACCGACAT GACTGTGCAC CTGATTCACC         800
        CGGTTGCCAT GGAGGATCAG CTCAAGTTCG CTA                           833
```

   55
        2) INFORMATION FOR SEQ ID NO: 146

            (i) SEQUENCE CHARACTERISTICS:
   60   (A)   LENGTH: 745 bases

```
           (B)    TYPE: Nucleic acid
           (C)    STRANDEDNESS: Double
           (D)    TOPOLOGY: Linear

 5    (ii)MOLECULE TYPE: Genomic DNA

      (vi)ORIGINAL SOURCE:
           (A)    ORGANISM: Proteus mirabilis
           (B)    STRAIN: ATCC 35659
10
         (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 146

      CACAAACTCG TGAGCACATC CTGTTAGGTC GTCAGGTTGG TGTTCCTTAC      50
      ATCATCGTAT TCCTGAACAA ATGTGACATG GTAGATGATG AAGAGCTGTT     100
15    AGAATTAGTT GAAATGGAAG TTCGTGAACT TCTGTCTCAA TACGATTTCC     150
      CAGGTGATGA CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCACTGGAA     200
      GGCGAAGCAG AGTGGGAAGC AAAAATTGTT GAATTAGCAG AAGCACTGGA     250
      TTCTTATATC CCAGAGCCAG AGCGTGCAAT TGACAAACCA TTCCTGTTAC     300
      CAATCGAAGA TGTATTCTCA ATCTCAGGCC GTGGTACAGT AGTTACTGGT     350
20    CGTGTAGAGC GTGGTATCAT CAAAGTAGGT GATGAAGTTG AGATTGTTGG     400
      TATCAAAGAA ACCGCCAAAA CAACTTGTAC TGGCGTTGAA ATGTTCCGTA     450
      AATTACTTGA CGAAGGTCGT GCAGGTGAGA ACGTAGGTGT TCTGCTGCGT     500
      GGTACAAAAC GTGAAGAAAT CGAACGTGGA CAAGTACTGG CRAAACCAGG     550
      CTCAATCAAC CCACACAACA AATTTGAATC AGAAGTTTAT ATTCTGAGCA     600
25    AAGATGAAGG TGGTCGTCAC ACTCCATTCT TCAAAGGCTA CCGTCCACAG     650
      TTCTACTTCC GTACAACTGA CGTAACTGGT ACTATCGAAT TACCAGAAGG     700
      CGTAGAAATG GTAATGCCAG GCGACAACGT GAACATGATC GTTGA          745


30
      2)INFORMATION FOR SEQ ID NO: 147

           (i)SEQUENCE CHARACTERISTICS:
           (A)    LENGTH: 829 bases
35         (B)    TYPE: Nucleic acid
           (C)    STRANDEDNESS: Double
           (D)    TOPOLOGY: Linear

         (ii)MOLECULE TYPE: Genomic DNA
40
         (vi)ORIGINAL SOURCE:
           (A)    ORGANISM: Proteus penneri
           (B)    STRAIN: ATCC 33519

45       (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 147

      GGAGCTATCC TGGTTGTTGC TGCGACAGAT GGCCCAATGC CACAAACTCG      50
      TGAGCACATC CTGTTAGGTC GTCAGGTTGG TGTTCCTTAC ATCATCGTAT     100
      TCCTGAACAA ATGTGACATG GTAGATGATG AAGAGTTACT GGAATTAGTM     150
50    GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC CAGGTGATGA     200
      CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCACTGGAA GGCGAAGCAG     250
      AGTGGGAAGC AAAAATTGTT GAATTAGCAG AAGCACTGGA TTCATACATC     300
      CCAGARCCAG AGCGTGCAAT TGACAAACCA TTCCTGTTAC CAATTGAAGA     350
      CGTATTCTCA ATTTCAGGCC GTGGTACAGT AGTAACAGGT CGTGTTGAGC     400
55    GTGGCGTAAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATTAAACCA     450
      ACAGCGAAAA CAACTTGTAC TGGCGTTGAA ATGTTCCGTA AATTACTTGA     500
      CGAAGGTCGT GCAGGTGAGA ACGTAGGTGT TCTTCTGCGT GGTACTAAAC     550
      GTGAAGAAAT CGAACGTGGA CAAGTACTGG CGAAACCAGG TTCAATCAAC     600
      CCACACACTA AATTTGAATC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG     650
60    TGGTCGTCAT ACTCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC     700
```

```
GTACAACTGA CGTAACTGGT ACTATCGAAT TACCAGAAGG CGTAGAAATG        750
GTAATGCCAG GTGACAACAT CAACATGATC GTTGAACTGA TTCACCCAAT        800
CGCGATGGAC GACGGTTTAC GTTTCGCTA                               829
```

2) INFORMATION FOR SEQ ID NO: 148

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 824 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Proteus vulgaris*
       (B)   STRAIN: ATCC 13315

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

```
CGGAGCTATT CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC        50
GTGAGCACAT CCTGTTAGGT CGCCAGGTTG GTGTACCTTA CATCATCGTA        100
TTCCTGAACA AATGTGACAT GGTTGATGAT GAAGAACTGC TGGAATTAGT        150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG        200
ACACTCCAGT AATCCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT        250
GAGTGGGAAG CAAAAATTGT TGAATTAGCA GAAGCACTGG ATTCTTACAT        300
CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCTATCGAAG        350
ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTAGAG        400
CGTGGTGTTG TTAAAGTTGG TGAAGAAGTT GAGATTGTTG GTATTAAAGA        450
CACAGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAATTACTTG        500
ACGAAGGTCG TGCAGGTGAG AACGTAGGTG TTCTTCTGCG TGGTACTAAA        550
CGTGAAGAAA TCGAACGTGG ACAAGTACTG GCTAAACCAG GTTCAATCAA        600
GCCACACACT AAATTCGAAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG        650
GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC        700
CGTACAACTG ACGTAACTGG TACTATCGAA TTACCAGAAG GCGTAGAAAT        750
GGTAATGCCA GGTGACAACA TCAACATGAT CGTTGAACTG ATTCACCCTA        800
TCGCGTAGGA CGACGGTTTA CGTT                                    824
```

2) INFORMATION FOR SEQ ID NO: 149

    (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 745 bases
       (B)   TYPE: Nucleic acid
       (C)   STRANDEDNESS: Double
       (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
       (A)   ORGANISM: *Providencia alcalifaciens*
       (B)   STRAIN: ATCC 9886

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

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CACAAACTCG TGAGCACATC CTGTTAGGTC GCCAAGTAGG TGTTCCTTAC        50
ATCATCGTTT TCCTGAACAA ATGTGACATG GTAGACGACG AAGAACTGTT        100
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90